

GenCore version 5.1.1.8
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OM protein - protein search, using sw model

Run on: May 25, 2006, 14:52:22 ; Search time 196 Seconds
(without alignments)
335.914 Million cell updates/sec

Title: US-10-614-481-9
Perfect score: 759
Sequence: 1 MWLQNLGLGTVYSMPAPT.....KNLKDFLFEIPDCWKPAQK 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*
10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	759	100.0	144	4 ABP98711	Abp98711 Equine gr
2	759	100.0	144	4 AAB37147	Aab37147 Equine gr
3	641	84.5	144	2 AAR23662	Aar23662 Ovine GM-
4	587	77.3	144	2 AAR54818	Aar54818 CHEF-2. 3
5	586	77.2	144	1 AAP60418	Aap60418 Human gra
6	586	77.2	144	1 AAP70657	Aap70657 Sequence
7	586	77.2	144	2 AAR04098	Aar04098 Metapycoc
8	586	77.2	144	2 AAR71118	Aar71118 GM-CSF en
9	586	77.2	144	2 AAR92800	Aar92800 Human GM-
10	586	77.2	144	2 AAW60031	Aaw60031 Human gra
11	586	77.2	144	3 AAB18633	Aab18633 Amino aci
12	586	77.2	144	4 AAB50871	Aab50871 Human GM-
13	586	77.2	144	4 AAB84602	Aab84602 Amino aci
14	586	77.2	144	5 ABB05055	Abb05055 Human gra
15	586	77.2	144	5 AAU11977	Aau11977 Human GM-
16	586	77.2	144	6 ABR55847	Abr55847 Human GM-
17	586	77.2	144	7 AAE14938	Aae14938 Human gra
18	586	77.2	144	7 ADF15243	Adf15243 Human alb
19	586	77.2	144	7 ADF15149	Adf15149 Human alb
20	586	77.2	144	7 ADF15242	Adf15242 Human alb
21	586	77.2	144	7 ADF15150	Adf15150 Human alb
22	586	77.2	144	7 ADH44684	Adh44684 Human GM-
23	586	77.2	144	7 ADI01020	Adi01020 Human gra

24	586	77.2	144	8 ADH10509	Adh10509 Human GM-
25	586	77.2	144	8 ADL66118	Adl66118 Human gra
26	586	77.2	144	8 ADL66120	Adl66120 Human PAP
27	586	77.2	144	8 ADL16730	Adl16730 Human gra
28	586	77.2	144	8 ADN07713	Adn07713 Human G-C
29	586	77.2	144	8 ADN49690	Adn49690 Human gra
30	586	77.2	144	8 ADP12451	Adp12451 Protein e
31	586	77.2	144	8 ADP19843	Adp19843 Human GMC
32	586	77.2	144	8 ADO59665	Ado59665 Human GMC
33	586	77.2	144	8 ADR46068	Adr46068 Human gra
34	586	77.2	144	8 ADR46066	Adr46066 Human gra
35	586	77.2	144	8 ADS88047	Ads88047 Tumour tr
36	586	77.2	144	8 ADU74366	Adu74366 Human gra
37	586	77.2	144	9 ADV96467	Adv96467 Human GM-
38	586	77.2	144	9 ADV19524	Adv19524 PRO polyp
39	586	77.2	144	9 ADY16395	Ady16395 PRO polyp
40	586	77.2	144	9 ADY84980	Ady84980 Human gra
41	586	77.2	144	9 ADZ26537	Adz26537 Human GMS
42	586	77.2	144	9 ADY99886	Ady99886 Human imm
43	586	77.2	144	9 ADZ20507	Adz20507 Human gra
44	586	77.2	144	9 AEB10855	Aeb10855 Human GM-
45	586	77.2	144	9 AEB54698	Aeb54698 Human col

ALIGNMENTS

RESULT 1
ID ABP98711 standard; protein; 144 AA.
XX
AC ABP98711;
XX
DT 27-JUN-2003 (first entry)
XX
DE Equine granulocyte-macrophage colony stimulating factor.

XX
KW Granulocyte-macrophage colony stimulating factor; GM-CSF; antibacterial;
KW antiviral; vaccine; animal; immunogen; DMR1E; cationic lipid; dog; cat;
KW quaternary ammonium salt; canine distemper virus; canine herpes virus;
KW canine parainfluenza virus; feline herpes virus; equine herpes virus;
KW horse.
XX
OS Equus caballus.
XX
PN WO200077043-A2.
XX
PD 21-DEC-2000.
XX
PF 08-JUN-2000; 2000WO-FR001592.
XX
PR 10-JUN-1999; 99FR-00007604.
XX
PR 19-JUL-1999; 99US-0144490P.
XX
(MERI-) MERIAL.
XX
PI Fischer LJ, Barzu-Le Roux S, Audonnet JF;
XX
DR WPI; 2001-071259/08.
XX
DR N-PSDB; ABZ80828.
XX
PT DNA vaccine containing plasmid and cationic lipid containing quaternary
PT ammonium salt, useful for protecting pets and sports animals against,
PT e.g. herpes virus.
XX
PS Example 10; Fig 26; 109pp; French.
XX
CC The invention relates to a novel DNA vaccine against pathogens that
CC affect pets and sports animals comprises a plasmid containing a sequence,
CC expressible in vivo, that encodes an immunogen from the relevant pathogen
CC and a cationic lipid containing a quaternary ammonium salt, particularly
CC N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium
CC (DMR1E). The immunogens are particularly taken from canine distemper

CC virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes
CC virus (CHV), feline herpes virus type 1 (FHV-1), equine herpes virus type
CC 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of
CC an immunogenic stimulation factor especially a granulocyte-macrophage
CC colony stimulation factor (GM-CSF) to enhance the immunogenic response.
CC The vaccines, which may be multivalent, are particularly used to protect
CC dogs, cats and horses against bacterial and viral diseases, particularly
CC those caused by the Paramyxoviridae. Formulations with the quaternary
CC ammonium salt provide a better immune response and thus more efficient
CC protection, particularly when administered subcutaneously. This sequence
CC represents an equine GM-CSF used in the invention
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 759; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.4e-74;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWLQNLLLLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLLNNSDSTAAMNETVEV 60
Db 1 MWLQNLLLLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLLNNSDSTAAMNETVEV 60
Qy 61 SETFDAEELTCLQTRLKLYKQGLRGLSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
Db 61 SETFDAEELTCLQTRLKLYKQGLRGLSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
Qy 121 KSFKKNLKDPLFEIPDFDCWKPAQK 144
Db 121 KSFKKNLKDPLFEIPDFDCWKPAQK 144

RESULT 2
AAB37147
ID AAB37147 standard; protein; 144 AA.

XX AAB37147;
XX
XX 18-JUN-2002 (first entry)
XX
XX Equine granulocyte-macrophage colony stimulating factor.
XX
XX Immunostimulatory; granulocyte-macrophage colony stimulating factor;
XX horse; reverse transcriptase PCR; colony formation; blood; cytotoxicity;
XX inflammation; vector; adjuvant; immunogen; vaccination; vaccine;
XX equine herpes; tetanus; Borrelia burgdorferi; rabies.
XX
OS Equus sp.
XX
XX WO200077210-A1.
XX
XX 21-DEC-2000.
XX
XX 08-JUN-2000; 2000WO-FR001590.
XX
XX 10-JUN-1999; 99US-0138843P.
XX
XX (MERI-) MERIAL.
XX
XX Bublot M, Perez JM, Andreoni CMP;
XX
XX WPI; 2001-080689/09.
XX
XX N-PSDB; AAF28953.
XX

XX Novel DNA encoding equine granulocyte-macrophage colony-stimulating
XX factor, useful as adjuvant for vaccines and as non-specific
XX immunostimulant.
XX
XX Claim 6; Fig 1; 34pp; French.
XX
XX This sequence represents a horse granulocyte-macrophage colony
XX stimulating factor (GM-CSF). The corresponding gene was isolated from
XX horse lymphocytes using a reverse transcriptase PCR method with primers
XX AAF28954-AAF28960. The protein has been shown to have at least 75%

CC homology with GM-CSF proteins from other animal species. GM-CSF induces
CC colony formation in various types of blood cells and particularly induces
CC cytotoxicity of macrophages; stimulates antibody-dependent cytotoxicity,
CC and causes recruitment of leucocytes to sites of inflammation. Vectors
CC containing the gene or the protein itself, are useful as adjuvants in
CC immunogenic or vaccinating compositions for horses, e.g. for protection
CC against equine herpes, tetanus, Borrelia burgdorferi, rabies etc. Also as
CC non-specific stimulators of the immune system. In a specific example,
CC plasmid pJP097, containing the sequence for equine GM-CSF was used to
CC transform CHO-K1 cells and the transformants grown for 48 hours. The
CC culture supernatant was then added to culture medium being used to grow
CC porcine bone marrow cells. After 14 days, the mean number of colonies per
CC culture box was 12-15, compared with none for cells grown in absence of
CC GM-CSF. Equine GM-CSF allows a reduction in the amount of
CC immunogenic/vaccinating component required, and may induce a response in
CC animals that would otherwise be non-responders
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 759; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.4e-74;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWLQNLLLLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLLNNSDSTAAMNETVEV 60
Db 1 MWLQNLLLLGTVVYVSMPTPTQPSVTPRPQHVDAIKEALSLLNNSDSTAAMNETVEV 60
Qy 61 SETFDAEELTCLQTRLKLYKQGLRGLSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
Db 61 SETFDAEELTCLQTRLKLYKQGLRGLSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
Qy 121 KSFKKNLKDPLFEIPDFDCWKPAQK 144
Db 121 KSFKKNLKDPLFEIPDFDCWKPAQK 144

RESULT 3
AAR23662
ID AAR23662 standard; protein; 144 AA.

XX AAR23662;
XX
XX 25-MAR-2003 (revised)
DT 27-OCT-1992 (first entry)
XX
XX Ovine GM-CSF.
XX
XX Granulocyte-macrophage colony-stimulating factor; immuno-depression;
KW vaccine adjuvants; cytokine.
XX
OS Ovis aries.

XX
XX Key Location/Qualifiers
FH Peptide 1..17
FT Peptide /note= "putative signal sequence"
FT Peptide 18..144
FT Peptide /note= "mature protein"

XX WO9205255-A.
XX
XX 02-APR-1992.
XX
XX 13-SEP-1990; 90AU-00002294.
XX
XX 13-SEP-1990; 90AU-00002294.
PR 21-MAR-1991; 91AU-00005175.
XX
XX (CSIR) COMMONWEALTH SCI & IND RES ORG.
XX
XX Wood PR, Rothel JS, Seow HF;
XX WPI; 1992-150483/18.
DR N-PSDB; AAQ24294.
DR

```

XX DNA encoding ovine cytokine(s) - used to prepare recombinant cytokine(s)
PT for treatment of immuno-depression in sheep.
PS Disclosure; Fig 3; 79pp; English.
XX
CC The sequence is that of the ovine granulocyte-macrophage colony
CC stimulating factor (GM-CSF), a cytokine-like molecule. The ovine
CC cytokines will be useful in the intensive livestock industries such as
CC live animal export trade, feed-lots and intensive rearing industries,
CC where animals are subjected to great environmental challenge with
CC infectious diseases, partic. respiratory infections, and are more prone
CC to immunodepressive effects. The cytokines may be used for treatment or
CC prophylaxis to maintain, stimulate or enhance immunoresponsiveness. They
CC may also be useful as natural adjuvants for vaccines for sheep and
CC cattle. See also AAR23661-R23667. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX Sequence 144 AA;
XX
XX Query Match 84.5%; Score 641; DB 2; Length 144;
XX Best Local Similarity 84.0%; Pred. No. 1.8e-61;
XX Matches 121; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
XX
XX QY 1 MWLQNLLLLGTVVYVSMPTPTQPSVTRPQHVDAIKEALSLLNNSDTAAIMNETVEV 60
XX Db 1 MWLQNLLLLGTVVCSFSAPTQPSVTRPQHVDAIKEALSLLNDSDTAAVMDTEV 60
XX
XX QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
XX Db 61 SEMFDSQPTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
XX
XX QY 121 KSFKKNLKDPLFEIPDFDCWPKPAQK 144
XX Db 121 KSFKENLKDPLFEIPDFDCWEPAQK 144
XX
XX RESULT 4
XX AAR54818
XX ID AAR54818 standard; protein; 144 AA.
XX AC AAR54818;
XX
XX DT 25-MAR-2003 (revised)
XX DT 10-MAR-2003 (revised)
XX DT 07-NOV-1994 (first entry)
XX
XX DE CHEF-2.
XX
XX KW Cytokine; chimerism enhancing factors; porcine; transplant;
XX KW xenogeneic cells; bone marrow; African swine fever; Hog cholera;
XX KW Pseudorabies.
XX
XX OS Sus scrofa.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..17
XX FT /note= "signal peptide"
XX
XX PN W09409803-A1.
XX
XX PD 11-MAY-1994.
XX
XX PF 26-OCT-1993; 93WO-US010295.
XX
XX PR 27-OCT-1992; 92US-00967188.
XX PR 08-OCT-1993; 93US-00133979.
XX
XX PA (BIOT-) BIOTRANSPLANT INC.
XX
XX PI Ponath PD, Rosa MD, Monroy RL, Schacter BZ, Hawley RJ;
XX WPI; 1994-167114/20.
XX

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DR N-PSDB; AAR64864.
XX
XX Porcine cytokine Chimerism Enhancing Factors (CHEFs) and DNA - used to
XX enhance xenograft tolerance.
XX
XX PS Claim 25; Page 72; 113pp; English.
XX
XX The sequence is that of a porcine cytokine designated chimerism enhancing
XX factor (CHEF-2). The cytokine can be used for improving engraftment,
XX stabilisation and proliferation of tissues, esp. bone marrow cells, in
XX xenogeneic transplantation. The cytokine may be used to prevent or treat
XX various swine diseases, e.g. African swine fever, Hog cholera,
XX Pseudorabies, etc. See also AAR54817-9. (Updated on 10-MAR-2003 to add
XX missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 144 AA;
XX
XX Query Match 77.3%; Score 587; DB 2; Length 144;
XX Best Local Similarity 76.4%; Pred. No. 1.4e-55;
XX Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;
XX
XX QY 1 MWLQNLLLLGTVVYVSMPTPTQPSVTRPQHVDAIKEALSLLNNSDTAAIMNETVEV 60
XX Db 1 MWLQNLLLLGTVVCSISAPTRPPSPVTRPQHVDAIKEALSLLNNSDTAAVNNETVDV 60
XX
XX QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
XX Db 61 CEMFDPQPTCVQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
XX
XX QY 121 KSFKKNLKDPLFEIPDFDCWPKPAQK 144
XX Db 121 KSFKDNLKFLFTIPDFDCWGPVK 144
XX
XX RESULT 5
XX AAP60418
XX ID AAP60418 standard; protein; 144 AA.
XX AC AAP60418;
XX
XX DT 25-MAR-2003 (revised)
XX DT 01-JAN-1980 (first entry)
XX
XX DE Human granulocyte macrophage-colony stimulating factor.
XX
XX KW Granulocyte; macrophage; colony stimulating factor; chemotherapy;
XX KW neoplastic disease therapy; infectious disease therapy; ss.
XX
XX OS Homo sapiens.
XX
XX PN W08603225-A.
XX
XX PD 05-JUN-1986.
XX
XX PF 18-NOV-1985; 85WO-US002250.
XX
XX PR 20-NOV-1984; 84US-00673898.
XX
XX PA (SCHE ) SCHERING BIOTECH CORP.
XX
XX PI Yokota T, Lee FD, Rennick D, Arai K;
XX WPI; 1986-155831/24.
XX
XX DR N-PSDB; AAN60364.
XX
XX New poly:peptide(s) for colony stimulation of granulocytes - useful for
XX enhancing body defences against neoplasms and infectious diseases and to
XX overcome myelo:suppression in chemotherapy.
XX
XX Disclosure; Fig 1; 53pp; English.
XX
XX The protein has GM-CSF activity and is useful in elucidating control
XX mechanisms of mammalian immune responses. It is also useful for
CC

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CC administration to enhance natural defences against neoplastic and
CC infectious diseases or as an adjunct in chemotherapy to overcome
CC myelosuppression. GM-CSF is prepared by conventional recombinant DNA
CC techniques. The factor has activity on human neutrophilic granulocytes,
CC macrophages and eosinophils. (Updated on 25-MAR-2003 to correct PF
CC field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 144 AA;

Query Match 77.2%; Score 586; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-55;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLNQLLLGLTVVYVSMPTQPSVTPRPMQHVDAIKEALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQSLLLGLTVVACISAPARSPSPSTQWHEVNAIQEARLLNLSRDTAAEMNETVEI 60

Qy 61 SETFDABELTCLQRLKLYKQGLRGLSLKLGPLTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQEPCTCLQRLKLYKQGLRGLSLKLGPLTMMASHYKQHCPTLETSCATQIITF 120

Qy 121 KSPFKNLKDFLFEIPFDCWKPAQK 144
Db 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 6
AAP70657
ID AAP70657; standard; protein; 144 AA.
XX
AC AAP70657;
XX
DT 18-APR-1991 (first entry)
XX
DE Sequence of a human granulocyte-macrophage colony stimulating factor (hGM
DE -CSF)-like polypeptide isolated from 5637 cell line.
XX
KW AIDS therapy; leukocyte; leukaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Cleavage-site 17..18
FT /note= "for signal peptide"
XX
FN W08702060-A.
PD 09-APR-1987.
XX
PF 03-OCT-1986; 86WO-US002106.
XX
PR 03-OCT-1985; 85US-00783414.
XX
PA (BIOJ) BIOGEN NV.
PA (DELA/) DELAMARTER J.
XX
PI Delamarter J, Ernst JF;
XX
DR WPI; 1987-108701/15.
DR N-PSDB; AAN71002.
XX
PT Human granulocyte-macrophage stimulating factor-like polypeptide(s) -
PT produced from recombinant DNA sequence having 5' terminal alteration.
XX
PS Example; Fig 2; 61pp; English.
XX
CC A recombinant DNA molecule encoding a hGM-CSF is claimed wherein there is
CC a 5' terminal alteration allowing higher yield than the native DNA
CC sequence. The cpds. may be used to reduce the likelihood of infections in
CC immunologically compromised individuals, such as those suffering from
CC AIDS by increasing their white blood cell count
XX
SQ Sequence 144 AA;

Query Match 77.2%; Score 586; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-55;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLNQLLLGLTVVYVSMPTQPSVTPRPMQHVDAIKEALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQSLLLGLTVVACISAPARSPSPSTQWHEVNAIQEARLLNLSRDTAAEMNETVEI 60

Qy 61 SETFDABELTCLQRLKLYKQGLRGLSLKLGPLTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQEPCTCLQRLKLYKQGLRGLSLKLGPLTMMASHYKQHCPTLETSCATQIITF 120

Qy 121 KSPFKNLKDFLFEIPFDCWKPAQK 144
Db 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 7
AAR04098
ID AAR04098 standard; protein; 144 AA.
XX
AC AAR04098;
XX
DT 10-SEP-1990 (first entry)
XX
DE Metapyrocatechase gene product.
XX
DE Metapyrocatechase; GM-CSF; leukopaenia; osteomyelodysplasia;
KW granulocyte macrophage colony stimulating factor; ds.
XX
OS Homo sapiens.
XX
PN JP02076596-A.
XX
PD 15-MAR-1990.
XX
PF 13-SEP-1988; 88JP-00229468.
XX
PR 13-SEP-1988; 88JP-00229468.
XX
PA (SAGA) SAGAMI CHEM RES CENTRE.
XX
DR WPI; 1990-128250/17.
DR N-PSDB; AAQ04017.
XX
PT Human granulocyte macrophage colony stimulating factor derivs. - useful
PT for treating diseases due to leukopenia or osteomyelo-dysplastic.
XX
PS Disclosure; Page ?; -pp; Japanese.
XX
CC Human GM-CSF derivs. have polypeptide fragment from N-terminal of
CC metapyrocatechase, bonded at its C-terminal to the N-terminal of GM-CSF.
CC Expression vectors pMGMI and pMGM3 also contain the tac promoter/operator
CC and the SD sequence of metapyrocatechase
XX
SQ Sequence 144 AA;

Query Match 77.2%; Score 586; DB 2; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-55;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLNQLLLGLTVVYVSMPTQPSVTPRPMQHVDAIKEALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQSLLLGLTVVACISAPARSPSPSTQWHEVNAIQEARLLNLSRDTAAEMNETVEI 60

Qy 61 SETFDABELTCLQRLKLYKQGLRGLSLKLGPLTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQEPCTCLQRLKLYKQGLRGLSLKLGPLTMMASHYKQHCPTLETSCATQIITF 120

Qy 121 KSPFKNLKDFLFEIPFDCWKPAQK 144
Db 121 ESFKENLKDFLLVIPFDCWEPVQE 144

[illegible]

19-MAR-2001 (first entry)
Human GM-CSF.

Human; zalpha31; alpha helical protein-31;
granulocyte-macrophage colony stimulating factor; GM-CSF; cytostatic;
anti-inflammatory; antiarthritic; antirheumatoid; immunosuppressive;
antiaesthetic; antibacterial; osteopathic; antiatherosclerotic;
antipsoriatic; dermatological; anti-HIV; gene therapy; osteoporosis;
Paget's disease; hyperparathyroidism; acute pancreatitis;
gastrointestinal disorder; inflammation; heart disorder; viral infection.

Homo sapiens.
WO200073458-A1.
07-DEC-2000.
26-MAY-2000; 2000WO-US014795.
28-MAY-1999; 99US-0136485P.
(ZMO) ZYMOGENETICS INC.
Conklin DC;
WPI; 2001-070967/08.
Novel 4-helix bundle cytokine, Zalpha31, useful for regulating the
function of immune system and for treating thyroid, adrenal, lymphoid,
inflammatory, pancreatic, blood or bone disorders.
Disclosure; Page 107-108; 111pp; English.

The present sequence is given in a specification relating to
polynucleotide and polypeptide molecules for mammalian secreted alpha
helical protein-31 (zalpha31). The polypeptides are a novel four-helix
bundle cytokine and may be used to regulate the functioning of the immune
system. The polypeptides are used to identify and isolate receptors
involved in spermatogenesis, steroidogenesis, testicular differentiation
and regulatory control of the hypothalamic-pituitary gonadal axis,
thyroid, heart and adrenal function. They are useful for treating
disorders of the reproductive system, thyroid, adrenal, heart and
immunological systems. Zalpha31 polypeptides, or antagonists are useful
in the treatment of e.g. osteoporosis, Paget's disease, and
hyperparathyroidism, acute pancreatitis and gastrointestinal disorders
and as analgesics, especially for bone pain. They can be used to treat
arthritis, eczema, scleroderma and other inflammatory diseases. The
polypeptides, nucleic acids and/or antibodies can be used to treat heart
disorders. They can limit infarct size following a heart attack, aid in
recovery after heart transplantation, treat complications related to poor
circulation e.g. diabetic foot ulcers, treat stroke, improve cardiac
function, induce skeletal muscle neogenesis and/or hyperplasia, be used
in kidney regeneration and/or for treating systemic and pulmonary
hypertension. Zalpha31 can be used for treating viral leukemias,
acquired immunodeficiency syndrome (AIDS) or gastrointestinal viral
infections

Sequence 144 AA;
Query Match 77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-55;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

1 MWLQNLGLGTVVYVSMPTPTQPSVTPRQWHDVAIKEALSLLNNSDPTAAIMNETVEVY 60
1 MWLQNLGLGTVVACISAPARSPSTQWVHNVAIQEARLLNLSRDTAAEMNETVEVI 60
61 SETFDABELTCLQTRLYKQGLRSLIKLEGPLTWMASHYKQHCPTLETSCATQMTTF 120
61 SEMFDLQEPCLQTRLEYKQGLRSLTKLKGFLTWMASHYKQHCPTPETSCATQITTF 120

121 KSFKKNLKDFLFEIPFDCWKPAQK 144
:|||||:|||||:|||||:|
121 ESFKENLKDFLLVIPFDCWEPVQE 144
:|||||:|||||:|||||:|

RESULT 13
AAB84602
ID AAB84602 standard; protein; 144 AA.
XX AAB84602;
AC AAB84602;
XX 05-SEP-2001 (first entry)
XX Amino acid sequence of granulocyte macrophage colony stimulating factor.
XX Growth factor; protein inhibitor; protease; damaged tissue;
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
KW vascular endothelial growth factor; urokinase plasminogen activator;
KW dermal ulcer; wound.
XX Homo sapiens.
XX OS
XX WO200149309-A2.
XX 12-JUL-2001.
XX 21-DEC-2000; 2000WO-IB001935.
XX 29-DEC-1999; 99GB-00030768.
XX (PFIZ) PFIZER LTD.
XX (PFIZ) PFIZER INC.
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
WPI. 2001-418351/44.
XX N-PSDB; AAH28217.
Composition for the treatment of damaged tissue i.e. chronic wounds and
dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
factor.
Disclosure; Page 548; 572pp; English.

The specification describes a pharmaceutical composition, comprising a
growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
inhibits the action of at least one specific adverse protein, i.e. a
protease, that is upregulated in a damaged tissue such as a wound
environment. Growth factors which are included in the composition of the
invention are platelet-derived growth factor (PDGF), fibroblast growth
factor (FGF), connective tissue derived growth factor (CTGF),
keratinocyte-derived growth factor (KGF), transforming growth factor-beta
(TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
and chrysalin. Inhibitors which are included in the composition of the
invention include inhibitors of urokinase-type plasminogen activator
(uPA) and matrix metalloproteinase (MMP). The composition is useful for
the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
The present sequence represents a human GM-CSF, and is used to produce
the composition of the invention

Sequence 144 AA;
Query Match 77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-55;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

1 MWLQNLGLGTVVYVSMPTPTQPSVTPRQWHDVAIKEALSLLNNSDPTAAIMNETVEVY 60
:|||||:|||||:|||||:|

Db 1 MWLQSLLLGTVACISAPARSPSTQPEWHVNAIQEARLLNLSRDTAAEMNETVEVI 60

Qy 61 SETDABELTCLQTRLKLYKQGLRSLIKLGGPLTMASHYKQHCPTLETSCATQMTIF 120

Db 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTLETSCATQIITF 120

Qy 121 KSEKKNLKDPLFEIPFDCWKPAOK 144

Db 121 ESFKENLKDFLLVFPDCWEPVQE 144

RESULT 14

ABBO5055

ID ABB05055 standard; protein; 144 AA.

XX

AC ABB05055;

DT 26-MAR-2002 (first entry)

XX Human granulocyte macrophage colony stimulating factor protein.

DE Human; granulocyte macrophage colony stimulating factor; GM-CSF;

XX fusion gene; glycoprotein; bladder specific promoter; uroplakin II.

KW Homo sapiens.

OS

XX KR2001077563-A.

FN 20-AUG-2001.

PD

XX 03-FEB-2000; 2000KR-00005437.

PF

XX 03-FEB-2000; 2000KR-00005437.

PR

XX (BIOC-) BIO CLUE & SOLUTION CO LTD.

PA (KIMT/) KIM T Y.

PI Byun SJ, Kim GE, Kim MO, Kim TY, Lee JU, Park YI, Ryu JU;

XX WPI; 2002-111646/15.

DR N-PSDB; ABA92719.

XX

XX Producing human granulocyte/macrophage colony-stimulating factor

PT comprises purifying the factor from the urine of a transformed animal.

XX

PS Disclosure; Page; 20pp; Korean.

XX

CC The present invention describes a method for producing human granulocyte

CC macrophage colony stimulating factor (hGM-CSF), where hGM-CSF having

CC higher activity is easily purified. The method comprises: (a) preparing a

CC fusion gene construct which contains a human origin glycoprotein gene

CC linked with a bladder specific promoter, uroplakin II; (b) microinjecting

CC the fusion gene construct into a fertilised egg; (c) transplanting the

CC egg containing the fusion gene construct (KCTC 0723BP) into a surrogate

CC mother; (d) producing a transformed animal from the surrogate mother; and

CC (e) purifying hGM-CSF from the urine of the transformed animal. The

CC present sequence represents hGM-CSF which is referred to using the

CC Genbank accession number X03021 in the exemplification of the present

CC invention. N.B. The present sequence is not given in the specification

XX

SQ Sequence 144 AA;

Query Match 77.2%; Score 586; DB 5; Length 144;

Best Local Similarity 76.4%; Pred. No. 1.8e-55;

Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQSLLLGTWVYXMPAPTRQPSVTRPWQHVDAIKEALLNNSSDTAIIMNETVEV 60

Db 1 MWLQSLLLGTVACISAPARSPSTQPEWHVNAIQEARLLNLSRDTAAEMNETVEVI 60

Qy 61 SETDABELTCLQTRLKLYKQGLRSLIKLGGPLTMASHYKQHCPTLETSCATQMTIF 120

Db 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTLETSCATQIITF 120

Qy 121 KSEKKNLKDPLFEIPFDCWKPAOK 144

Db 121 ESFKENLKDFLLVFPDCWEPVQE 144

RESULT 15

AAU11977

ID AAU11977 standard; protein; 144 AA.

XX

AC AAU11977;

DT 09-APR-2002 (first entry)

XX Human GM-CSF polypeptide.

DE

XX Cytokine; zalphall ligand; zalphall receptor; NK cell progenitor;

KW natural killer cell proliferation; T-cell proliferation; human;

XX B-cell proliferation; anti-tumour response; immune system; GM-CSF;

KW immunostimulant; granulocyte macrophage-colony stimulating factor.

XX

OS Homo sapiens.

XX US6307024-B1.

FN 23-OCT-2001.

PD

XX 09-MAR-2000; 2000US-00522217.

PF

XX 09-MAR-1999; 99US-0123547P.

PR 11-MAR-1999; 99US-0123904P.

PR 01-JUL-1999; 99US-0142013P.

XX (ZYMO) ZYMOGENETICS INC.

PA Novak JE, Presnell SR, Sprecher CA, Foster DC, Holly RD;

XX Gross JA, Johnston JV, Nelson AJ, Dillon SR, Hammond AK;

PI WPI; 2002-040208/05.

DR

XX New zalphall ligand polypeptides and polynucleotides, useful for

PT stimulating proliferation, activation, differentiation and/or induction

PT of inhibition of specialized cell function, or for stimulating an

PT antigenic response.

XX

PS Disclosure; Col 191-192; 105pp; English.

XX

CC The present invention relates to the isolation of a novel cytokine,

CC zalphall ligand and the polynucleotide encoding it. The invention also

CC gives the sequence for the zalphall receptor and the polynucleotide

CC encoding it. The zalphall ligand polypeptide stimulates proliferation of

CC natural killer (NK) cells or NK cell progenitors, the activation of NK

CC cells, proliferation of T-cells, proliferation of B-cells stimulated with

CC anti-CD40 antibodies, stimulates an antigenic response in a mammal, and

CC reduces proliferation of B-cells stimulated with anti-IGM antibodies. The

CC zalphall ligand polypeptide is also useful in preparing antibodies that

CC bind to zalphall ligand epitopes. The zalphall ligand polynucleotides can

CC be used as probes or primers to clone regions of a zalphall ligand gene,

CC and in gene therapy. Zalphall ligand may also be used to identify

CC inhibitors of its activity, to enhance the generation of anti-tumour

CC responses with or without the infusion of donor lymphocytes, and to

CC activate or stimulate the immune system. The present sequence

CC representing human GM-CSF (granulocyte macrophage-colony stimulating

CC factor) polypeptide can be used to create fusion proteins containing

CC helix regions from the human zalphall ligand polypeptide and from the

CC present polypeptide

XX

SQ Sequence 144 AA;

Query Match 77.2%; Score 586; DB 5; Length 144;

Best Local Similarity 76.4%; Pred. No. 1.8e-55;

Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: May 25, 2006, 14:56:07 ; Search time 39 Seconds
(without alignments)
355.262 Million cell updates/sec

Title: US-10-614-481-9
Perfect score: 759
Sequence: 1 MWLQNLLLLGTWVYVSMAPT.....KNLKDFLFEIPDCWKPAQK 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	641	84.5	144	1 A61632	granulocyte-macrop
2	637	83.9	144	2 JH0469	granulocyte-macrop
3	586	77.2	144	1 FQHUGM	granulocyte-macrop
4	574.5	75.7	143	1 FQBOGM	granulocyte-macrop
5	566	74.6	144	2 A44936	granulocyte-macrop
6	450.5	59.4	153	1 FQMSGM	granulocyte-macrop
7	448	59.0	127	2 I46269	granulocyte-macrop
8	84.5	11.1	660	2 T39964	hypothetical coile
9	81.5	10.7	424	2 F69476	acetylornithine am
10	79.5	10.5	913	1 B42543	DNA-directed DNA p
11	78.5	10.3	397	2 F97707	acyl-CoA desaturas
12	78.5	10.3	400	2 G90465	acyl-CoA dehydroge
13	78.5	10.3	760	2 S70294	FUN21 protein - ye
14	78.5	10.3	943	2 E84429	probable receptor-
15	77	10.1	490	2 A96556	probable tRNA-guan
16	77	10.1	901	2 F86833	phage infection pr
17	76.5	10.1	913	2 T17675	DNA-directed DNA p
18	76	10.0	311	2 G86383	probable mitochond
19	76	10.0	560	2 A48724	hexose transport p
20	75	9.9	389	2 S53612	gene MSP-2 protei
21	74.5	9.8	1276	2 T18526	SREP cleavage act
22	74	9.7	1607	2 T03022	MAP kinase kinase
23	73.5	9.7	187	2 B83695	hypothetical prote
24	73.5	9.7	193	2 G83901	hypothetical prote
25	73	9.6	901	2 A48653	phage infection pr
26	72.5	9.6	394	2 S36512	E2 protein - human
27	72.5	9.6	474	2 T20706	hypothetical prote
28	72.5	9.6	674	2 S75662	sensory transducti
29	72.5	9.6	913	1 A42543	DNA-directed DNA p

30 9.5 167 2 F84559 histone H1 [import
31 72 187 2 H81979 hypothetical prote
32 72 9.5 884 2 B96492 probable polypept
33 72 9.5 1127 2 T30334 AND-1 protein - AF
34 72 9.5 1364 2 T10236 xanthine dehydroge
35 72 9.5 1450 2 T30273 hypothetical prote
36 71 9.4 208 2 J80512 fusaric acid resis
37 71 9.4 312 2 G87536 hypothetical prote
38 71 9.4 591 2 F64334 acetolactate synth
39 71 9.4 644 2 A42220 helix-loop-helix p
40 71 9.4 769 2 S54525 mismatch repair pr
41 71 9.4 828 2 D81522 DNA mismatch repai
42 71 9.4 828 2 C86608 DNA mismatch repai
43 71 9.4 828 2 G72017 probable chitinase
44 71 9.4 1088 2 D82246 myosin VII-like pr
45 71 9.4 2121 2 A59233

ALIGNMENTS

RESULT 1

A61632

granulocyte-macrophage colony-stimulating factor precursor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A61632

R:O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.

Immunol. Cell Biol. 69, 51-55, 1991

A:Title: Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stim

A:Reference number: A61632; MUID:91331592; PMID:1869289

A:Accession: A61632

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-144 <OAB>

A:Cross-references: UNIPROT:Q9MYK4; UNIPARC:UPI000008836D; GB:X55991; NID:G6983759; PIDN

C:Superfamily: granulocyte-macrophage colony-stimulating factor

F,1-17/Domain: signal sequence #status predicted <SIG>

Query Match 84.5%; Score 641; DB 1; Length 144;
Best Local Similarity 84.0%; Pred. No. 3.9e-54;
Matches 121; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MWLQNLLLLGTWVYVSMAPTROPSPVTRPQHVDAIKEALSLNNSSDTAAIMNETVEVV 60

Db 1 MWLQNLLLLGTWVYVSMAPTROPSPVTRPQHVDAIKEALSLNNSSDTAAIMNETVEVV 60

Qy 61 SETFDABEILTCLQTRKLYKQGLRGLSLKLEGLPTMMASHYKQHCPTTLETSCATQMIITF 120

Db 61 SEMFDSQEPTECLQTRLELYKQGLRGLSLTSLGSLTMMASHYKQHCPTTLETSCATQMIITF 120

Qy 121 KSFKNLKDFLFEIPDCWKPAQK 144

Db 121 KSFKNLKDFLFEIPDCWKPAQK 144

RESULT 2

JH0469

granulocyte-macrophage colony-stimulating factor precursor - sheep

N:Alternate names: colony-stimulating factor 2; GM-CSF

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C:Accession: JH0469; S16730

R:McInnes, C.J.; Haig, D.M.

Gene 105, 275-279, 1991

A:Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-st

A:Reference number: JH0469; MUID:92039044; PMID:1937025

A:Accession: JH0469

A:Molecule type: mRNA

A:Residues: 1-144 <MCI>

A:Cross-references: UNIPROT:P28773; UNIPARC:UPI0000128522; GB:X53561; NID:G1800; PIDN:CA

C:Comment: This protein is a glycoprotein cytokine produced and secreted by various cell

C:Superfamily: granulocyte-macrophage colony-stimulating factor

C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA
F;44/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.9%; Score 637; DB 2; Length 144;
Best Local Similarity 83.3%; Pred. No. 9,4e-54;
Matches 120; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MWLQNLLLGTVVYVSMPTPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQNLLLGTVVCSFSAPTQPSVTPRWQHVDAIKEALSLLNDSDTAAVMDTEV 60

Qy 61 SETPDABELTCLQRLKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDSQPTCLQTRLELYKQGLRSLTSLTGLTMMASHYKHCPTQETSCETQIITF 120

Qy 121 KSFKKNLKDFLFEIPDFDCWKPAOK 144
Db 121 KSFKENLKDFLFIIPDFCWEVQK 144

RESULT 3
FOHUGM
granulocyte-macrophage colony-stimulating factor precursor [validated] - human
N;Alternate names: colony-stimulating factor 2; GM-CSF
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: C24636; I59065; A25169; A01853; A44175; JCI1090
R;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
EMBO J. 4, 2561-2568, 1985

A;Title: Structure of the chromosomal gene for granulocyte-macrophage colony stimulating
A;Reference number: A91015; MUID:86030234; PMID:3876930
A;Accession: C24636
A;Molecule type: DNA
A;Residues: 1-144 <MIV>
A;Cross-references: UNIPROT:P04141; UNIPARC:UPI00000358DB; EMBL:X03021; NID:g31858; PIDN
R;Kaushansky, K.; O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hagen, F.S.; Adamson, J.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 3101-3105, 1986

A;Title: Genomic cloning, characterization, and multilineage growth-promoting activity o
A;Reference number: I59065; MUID:86205844; PMID:3486413
A;Accession: I59065
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-144 <RES>
A;Cross-references: UNIPARC:UPI00000358DB; GB:M13207; NID:g181147; PIDN:AAA98768.1; PID:
R;Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R.
Proc. Natl. Acad. Sci. U.S.A. 82, 6250-6254, 1985

A;Title: Cloning, sequence, and expression of a human granulocyte/macrophage colony-stim
A;Reference number: A25169; MUID:85298329; PMID:3898082
A;Accession: A25169
A;Molecule type: mRNA
A;Residues: 1-144 <CAN>
A;Cross-references: UNIPARC:UPI00000358DB; GB:M11734; NID:g181149; PIDN:AAA52122.1; PID:
R;Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.; Luh, J.; Arai, K.; Rennick,
Proc. Natl. Acad. Sci. U.S.A. 82, 4360-4364, 1985

A;Title: Isolation of cDNA for a human granulocyte-macrophage colony-stimulating factor
A;Reference number: A01853; MUID:85242684; PMID:3925454
A;Accession: A01853
A;Molecule type: mRNA
A;Residues: 1-144 <LEE>
A;Cross-references: UNIPARC:UPI00000358DB; GB:M11220; NID:g183363; PIDN:AAA52578.1; PID:
R;Wong, G.G.; Witek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary, A.C.; Luxenberg, D.P.; JC
A.; Clark, S.C.
Science 228, 810-815, 1985

A;Title: Human GM-CSF: molecular cloning of the complementary DNA and purification of th
A;Reference number: A44175; MUID:85218749; PMID:3923623
A;Accession: A44175
A;Molecule type: mRNA
A;Residues: 1-116, 'T', 118-144 <NON>
A;Cross-references: UNIPARC:UPI0000142467; GB:M10663; NID:g181145; PIDN:AAA52121.1; PID:
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Wen, D.Y.; Huang, B.R.; Cai, L.W.; Si, J.Y.

Acta Biochim. Biophys. Sin. 25, 651-655, 1993
A;Title: Amplification of human granulocyte-macrophage colony-stimulating factor cDNA wit
A;Reference number: JCI1090
A;Accession: JCI1090
A;Molecule type: protein
A;Residues: 18-21, 'C', 23-96, 'L', 98-144 <WEN>
A;Cross-references: UNIPARC:UPI000017368E
C;Genetics: GDB:CSF2
A;Gene: GDB:CSF2
A;Cross-references: GDB:119812; OMIM:138960
A;Map position: 5q23.2-5q31.1
A;Introns: 53/3; 67/3; 109/3
C;Function:
A;Description: stimulates the differentiation and proliferation of hematopoietic progeni
C;Superfamily: granulocyte-macrophage colony-stimulating factor
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status experimental <
F;44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 77.2%; Score 586; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 7.1e-49;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLLLGTVVYVSMPTPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQSLLLGTVVACISAPARSPSPSTQPSWQHVDAIQEARLLNLRSRTAAEMNETVEV 60

Qy 61 SETPDABELTCLQRLKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLGLPTMMASHYKQHCPTPETSCATQIITF 120

Qy 121 KSFKKNLKDFLFEIPDFDCWKPAOK 144
Db 121 ESFKENLKDFLFIIPDFCWEVQK 144

RESULT 4
FOBOGM
granulocyte-macrophage colony-stimulating factor precursor - bovine
N;Alternate names: colony-stimulating factor 2; GM-CSF
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: JI0037
R;Maliszewski, C.R.; Schoenborn, M.A.; Cerretti, D.P.; Wignall, J.M.; Picha, K.S.; Cosmar
Mol. Immunol. 25, 843-850, 1988

A;Title: Bovine GM-CSF: molecular cloning and biological activity of the recombinant prot
A;Reference number: JI0037; MUID:89096971; PMID:3062386
A;Accession: JI0037
A;Molecule type: mRNA
A;Residues: 1-143 <MAL>
A;Cross-references: UNIPROT:P11052; UNIPARC:UPI000012851C
C;Comment: This glycoprotein induces granulocyte, macrophage, and eosinophil colony forma
C;Superfamily: granulocyte-macrophage colony-stimulating factor
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-143/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA
F;44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 75.7%; Score 574.5; DB 1; Length 143;
Best Local Similarity 75.7%; Pred. No. 8.9e-48;
Matches 109; Conservative 16; Mismatches 18; Indels 1; Gaps 1;

Qy 1 MWLQNLLLGTVVYVSMPTPTQPSVTPRWQHVDAIKEALSLLNNSDTAAIMNETVEV 60
Db 1 MWLQNLLLGTVVCSFSAPTPTATPTRWQHVDAIKEALSLLNHSDDTDAVMNDT-EV 59

Qy 61 SETPDABELTCLQRLKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120
Db 60 SEKFDSDQPTCLQTRKLYKQGLQSLTSLMWSLTMATHYKHCPTPETSCGTQFISF 119

Qy 121 KSFKKNLKDFLFEIPDFDCWKPAOK 144
Db 121 ESFKENLKDFLFIIPDFCWEVQK 144

Matches 82; Conservative 16; Mismatches 29; Indels 0; Gaps 0;
Qy 18 APTQPSVTPRQWQVDAIKALSLLNNSDTAAIMNETVEVSTFPAEELTCLQTRLK 77
Dy 1 APTQSPNVPTRPWKHVDAIKALSLLNDRALENEKNEVDIISNEFSIQRPCTVCQTRLK 60
Qy 78 LYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITFKSKKNLKDPLFEIPDF 137
Dy 61 LYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITFKSKKNLKDPLFEIPDF 120
Qy 138 CWKPAQK 144
Dy 121 CWKPVQK 127
RESULT 8
T39964
hypotheical coiled-coil protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39964
R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Wambutt, R.; Wedler, R.;
submitted to the EMBL Data Library, June 1998
A:Reference number: 221894
A:Accession: T39964
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-660 <LYN>
A:Cross-references: UNIPROT:Q60187; UNIPARC:UPI0000135984; EMBL:AL023779; PIDN:CAA19316.
A:Experimental source: strain 972h-; cosmid c244
C:Genetics:
A:Gene: SPDB:SPBC244.01c
A:Map position: 2
A:Introns: 39/1

Query Match 11.1%; Score 84.5; DB 2; Length 660;
Best Local Similarity 24.2%; Pred. No. 4.4;
Matches 40; Conservative 22; Mismatches 52; Indels 51; Gaps 6;
Qy 3 LQNL-LLLGTVVYMPAP-----TRQSPVTPRQWQVDAIKALSLLNN---SSPTA 50
Dy 248 LQNRNVHLETPEVPPVPGVPLTSSVCVSSISQPIQSTDCQKAQENLNKQMSNDQ 307
Qy 51 AI-----MNETVEVSTFPAEELTCLQTRLKLYKQGLRSLIKL 90
Dy 308 DIDPPKQAITDLPSPFVNVLEMNATIOQLSNQ-----CQQRDK-----OI 348
Qy 91 EGPLTMASHYKQHCPTLETSCATQMITFKSKKNLKDPLFEIP 135
Dy 349 ENITKQLLMNODYCPTTMTSTVSTPLCPKRPKSTKDFKEQK 393

RESULT 9
F69476
acetylornithine aminotransferase (argD-2) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: F69476
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: F69476
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-424 <KLE>
A:Cross-references: UNIPROT:P56969; UNIPARC:UPI000005689F; GB:AE000977; GB:AE000782; NID
C:Superfamily: beta-alanine-pyruvate transaminase

Query Match 10.7%; Score 81.5; DB 2; Length 424;
Best Local Similarity 27.3%; Pred. No. 5.1;
Matches 42; Conservative 15; Mismatches 52; Indels 45; Gaps 8;
Qy 7 LLLGTVVYMPAPTRQSPVTPRQWQVDAIKALSLLNNSDTAAIMNETVEV----- 59
Dy 154 LAAGDEKYRKPFEPPLAPGFEVPPGDAEAVEKAV-----DDDTAAVLFTETIPATLGMPLP 208
Qy 60 -----VSETFDABELTCL-----QTRLKLYKQGLRSLIKLEGPLTMASHYKQHC 106
Dy 209 PEDFYRRVREICD--EKGLMIMDEVQTGL-----GRTGKMWGIE-----HYKV-VP 252
Qy 107 PTLET---SCATQMITFKSKKNLKDPLFEIPF 136
Dy 253 DVIIVAKLSGGVYPISATCFKGLDLPFAENPFF 286

RESULT 10
B42543
DNA-directed DNA polymerase (EC 2.7.7.7) - Chlorella virus CV-NY-2A
C:Species: Chlorella virus CV-NY-2A
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 27-Oct-2003
C:Accession: B42543
R:Grabherr, R.; Strasser, P.; Van Etten, J.L.
Virolgy 188, 721-731, 1992
A:Title: The DNA polymerase gene from chlorella viruses PBCV-1 and NY-2A contains an intr
A:Reference number: A42543; MUID:92263776; PMID:1585643
A:Accession: B42543
A:Molecule type: DNA
A:Residues: 1-913 <GRA>
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C:Genetics:
A:Introns: 682/3
C:Superfamily: DNA polymerase
C:Keywords: DNA binding; DNA biosynthesis; DNA replication; exonuclease; nucleotidyltran
F:182-199/Region: exonuclease pattern A
F:268-282/Region: exonuclease pattern B
F:388-401/Region: exonuclease pattern C

Query Match 10.5%; Score 79.5; DB 1; Length 913;
Best Local Similarity 28.3%; Pred. No. 19;
Matches 26; Conservative 8; Mismatches 35; Indels 23; Gaps 2;
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Dy 722 RDFSPTIR-----ELKESLDTILFKDTPFAVETVESCIRKVDNEIPMEKFTMSKTLK 776
Qy 81 QGLRSLIKLEGPLTMASHYKQHCPTLET 112
Dy 777 TG-----YKNECQPHLHVS 790

RESULT 11
F97707
acyl-CoA desaturase 1 [imported] - Rickettsia conorii (strain Malish 7)
C:Species: Rickettsia conorii
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 05-Oct-2004
C:Accession: F97707
R:Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; Ro
Science 293, 2093-2098, 2001
A:Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A:Reference number: A97700; MUID:21442074; PMID:11557893
A:Accession: F97707
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <KUR>
A:Cross-references: UNIPROT:Q92JK5; UNIPARC:UPI000000C8C8D; GB:AE006914; PIDN:AAL02600.1;
C:Genetics:
A:Gene: acol
C:Superfamily: acyl-CoA desaturase
Query Match 10.3%; Score 78.5; DB 2; Length 397;
Best Local Similarity 24.8%; Pred. No. 9.1;

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A:Cross-references: UNIPARC:UPI0000179F9; EMBL:U12980; MIPS:YAL031C
A:Note: this sequence has been revised in reference S70291
A:Accession: S53563
A:Molecule type: DNA
A:Residues: 1-96, 'KVP', 104, 'A', 106, 'SIPADKAK', 115, 'SAAEI', 121, 'N' <BUF>
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A:Note: this sequence has been revised in reference S70291
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A:Gene: SGD:FUN21
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A:Map position: 1L
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C:Keywords: transmembrane protein
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F:194-210/Domain: transmembrane #status predicted <TM2>
F:287-303/Domain: transmembrane #status predicted <TM3>

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Db 596 STNPSASSLAPSPKVSINNTSSGKSSSTLIANSSDTLAI--ETLTDPES-NSSELS 652

Qy 71 CLQTRLKLYKQGLRGLSLIKLEGPLTMMASHYKQ----HCPPTLETSCATQMITFKS---- 122
Db 653 IKRVRF----AGV-PPMTEAENPKTKVGWYKKPAVLHYPP-IPASAMIKPLQHKSKYNT 706

Qy 123 -----FKNLDKDFL 131
Db 707 LRQEGFTFRKSLRDGL 723

RESULT 14
E84429
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 31-Dec-2004
C:Accession: E84429
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; A
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: R84420; MUID:20083487; PMID:10617197
A:Accession: E84429
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-943 <STO>
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C:Genetics:
A:Gene: At2g01820
A:Map position: 2
C:Superfamily: Receptor-like protein kinase; leucine-rich alpha-2-glycoprotein repeat hom

Query Match 10.3%; Score 78.5; DB 2; Length 943;
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Matches 21; Conservative 10; Mismatches 23; Indels 5; Gaps 2;

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Db 150 PWVIPDTVKATSLQNLTLSNCSIIIGK---IPDFGSQLPSL-TNLKLSQNGLEGEL 203

RESULT 15
A96556
probable trNA-guanine transglycosylase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004
C:Accession: A96556
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A96556
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-490 <STO>
A:Cross-references: UNIPROT:Q9C8H9; UNIPARC:UPI00000A4D88; GB:AE005173; NID:g11094755; F
C:Genetics:
A:Gene: F19C24.8
A:Map position: 1
C:Superfamily: Ubiquitin carboxyl-terminal hydrolase

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Matches 38; Conservative 14; Mismatches 53; Indels 38; Gaps 6;

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Db 191 WTQ---LTYLTSQSLKAPTSS-----EGADAVKALFGVNLQSRIKLGVLDNVTDSTV 239
Qy 52 I-----MNETVEVVSETFDAEELTC-----LQTRLKLYKQGLRGLKLEGPLTWM 97
Db 240 ISKCTLHCQESGESESESVSLKCHISHEVNHLEGL---KHGLKGELEKTSFALGRT 296
Qy 98 ASHYKQHCPTLETSCATQMITF 120
Db 297 ALYVKESLIDSLPYLTQFVRF 319

Search completed: May 25, 2006, 15:01:36
Job time : 41 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:01:52 ; Search time 599 Seconds
(without alignments)
367.081 Million cell updates/sec

Title: US-10-614-481-9

Perfect score: 759

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 8366291 seqs, 1526956180 residues

Total number of hits satisfying chosen parameters: 8366291

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	759	100.0	144	25	US-09-587-964-8	Sequence 8, Appl
2	759	100.0	144	25	US-09-587-964A-8	Sequence 8, Appl
3	759	100.0	144	36	US-10-614-481-9	Sequence 9, Appl
4	759	100.0	146	43	US-11-301-800-10	Sequence 10, Appl
5	641	84.5	144	27	US-09-791-537-98077	Sequence 98077, A
6	637	83.9	144	27	US-09-791-537-55369	Sequence 55369, A
7	633	83.4	144	27	US-09-791-537-69622	Sequence 69622, A
8	633	83.4	144	43	US-11-301-800-15	Sequence 15, Appl
9	597	78.7	144	27	US-09-791-537-82598	Sequence 82598, A
10	587	77.3	144	27	US-09-791-537-101680	Sequence 101680, A
11	587	77.3	144	43	US-11-301-800-12	Sequence 12, Appl
12	586	77.2	144	1	PCT-US00-00667-114	Sequence 114, Appl
13	586	77.2	144	1	PCT-US02-3263-18	Sequence 18, Appl
14	586	77.2	144	1	PCT-US02-34502-10	Sequence 10, Appl
15	586	77.2	144	1	PCT-US02-40891-447	Sequence 447, App
16	586	77.2	144	1	PCT-US02-40891-448	Sequence 448, App
17	586	77.2	144	1	PCT-US02-40891-540	Sequence 540, App
18	586	77.2	144	1	PCT-US02-40891-541	Sequence 541, App
19	586	77.2	144	1	PCT-US03-12946-2460	Sequence 2460, Ap
20	586	77.2	144	1	PCT-US03-17808-10	Sequence 10, Appl
21	586	77.2	144	1	PCT-US03-29176-3	Sequence 3, Appl
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25	586	77.2	144	1	PCT-US04-11494-18	Sequence 18, Appl
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27	586	77.2	144	1	PCT-US04-31524-163	Sequence 163, App
28	586	77.2	144	1	PCT-US05-00518-24	Sequence 24, Appl
29	586	77.2	144	11	US-08-105-215-7	Sequence 7, Appl
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33	586	77.2	144	27	US-09-726-295-15	Sequence 15, Appl
34	586	77.2	144	27	US-09-791-537-55367	Sequence 55367, A
35	586	77.2	144	31	US-10-116-275-217	Sequence 217, App
36	586	77.2	144	31	US-10-131-985-15	Sequence 15, Appl
37	586	77.2	144	31	US-10-170-205E-39311	Sequence 39311, A
38	586	77.2	144	32	US-10-287-994-18	Sequence 18, Appl
39	586	77.2	144	33	US-10-331-755-27	Sequence 27, Appl
40	586	77.2	144	34	US-10-410-897-18	Sequence 18, Appl
41	586	77.2	144	34	US-10-410-930-18	Sequence 18, Appl
42	586	77.2	144	34	US-10-410-945-18	Sequence 18, Appl
43	586	77.2	144	34	US-10-410-962-18	Sequence 18, Appl
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45	586	77.2	144	34	US-10-410-980-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1

US-09-587-964-8
; Sequence 8, Application US/09587964
; GENERAL INFORMATION:

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; APPLICANT: Fischer, et al.
; TITLE OF INVENTION: IMPROVED DNA VACCINES FOR PETS
; FILE REFERENCE: 454313-2530.1
; CURRENT APPLICATION NUMBER: US/09/587,964
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 60/144,490
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Equus sp.
US-09-587-964-8

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Best Local Similarity 100.0%; Pred. No. 4.3e-77;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
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; TITLE OF INVENTION: IMPROVED DNA VACCINES FOR PETS
; FILE REFERENCE: 454313-2530.1
; CURRENT APPLICATION NUMBER: US/09/587,964A
; CURRENT FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: US 60/144,490
; PRIOR FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.0
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; TYPE: PRT
; ORGANISM: Equus sp.
US-09-587-964A-8

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RESULT 3
US-10-614-481-9
; Sequence 9, Application US/10614481
; GENERAL INFORMATION:
; APPLICANT: Bublot, et al.

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; TITLE OF INVENTION: Equine GM-CSF
; FILE REFERENCE: 454313-2334.1
; CURRENT APPLICATION NUMBER: US/10/614,481
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/589,460
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/138,843
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 9
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US-10-614-481-9

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QY 1 MWLQNLGTVVYVSMPTPTQPSVTRPQHVDAIKEALSLLNNSDTAAIMNETVEV 60
DB 1 MWLQNLGTVVYVSMPTPTQPSVTRPQHVDAIKEALSLLNNSDTAAIMNETVEV 60
QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
QY 121 KSFKKNLKDFLFEIPFDCWKPAQK 144
DB 121 KSFKKNLKDFLFEIPFDCWKPAQK 144

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RESULT 4
US-11-301-800-10
; Sequence 10, Application US/11301800
; GENERAL INFORMATION:
; APPLICANT: BUELOW, ROLAND
; APPLICANT: PLAIZER, JOSEF
; TITLE OF INVENTION: IMPROVED DNA IMMUNIZATION WITH
; FILE REFERENCE: RECOMBINASE/TRANSPORASE
; FILE REFERENCE: 39691-0013
; CURRENT APPLICATION NUMBER: US/11/301,800
; CURRENT FILING DATE: 2005-12-12
; PRIOR APPLICATION NUMBER: US 60/636,361
; PRIOR FILING DATE: 2004-12-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Equus
US-11-301-800-10

Query Match      100.0%; Score 759; DB 43; Length 146;
Best Local Similarity 100.0%; Pred. No. 4.4e-77;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MWLQNLGTVVYVSMPTPTQPSVTRPQHVDAIKEALSLLNNSDTAAIMNETVEV 60
DB 1 MWLQNLGTVVYVSMPTPTQPSVTRPQHVDAIKEALSLLNNSDTAAIMNETVEV 60
QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
QY 121 KSFKKNLKDFLFEIPFDCWKPAQK 144
DB 121 KSFKKNLKDFLFEIPFDCWKPAQK 144

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RESULT 5
US-09-791-537-98077

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; AFFILIATION: DUNZEL, JOSEPH
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 98077
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-791-537-98077

```

Query Match	84.5%	Score 641;	DB 27;	Length 144;
Best Local Similarity	84.0%;	Pred. No. 1.1e-63;		
Matches 121;	Conservative 11;	Mismatches 12;	Indels 0;	Gaps 0;
QY 1	MWLNQLLLGLGTVVYVMPAPTRQPSVPTRPQHVDAI	KEALLNNSDDTA	RAIMNTEVVV	60
DB 1	MWLNQLLLGLGTVVCSAPTRQPSVPTRPQHVDAI	KEALLNNSDDT	TAHVMDTEVVV	60
QY 61	SETFDAAELTCLQTRKLKYQGRGSLIKLEGPLT	WMASHYKHCPPTLET	SCATQMITF	120
DB 61	SEMFDSQEPCTQLTRLELYKQGRGSLTSLTGS	LTWMASHYKHCPPTQ	TSETQIITF	120
QY 121	KSPKKNLKFLEIPFDCKWPAOK	144		
DB 121	KSPKENLKFLEIPFDCKWPAOK	144		

```

US-09-791-537-55369
; Sequence 55369, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 55369
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-791-537-55369

```

	Query Match	83.9%	Score 637;	DB 27;	Length 144;
	Best Local Similarity	83.3%;	Pred. No. 3.1e-63;		
	Matches 120;	Conservative 11;	Mismatches 13;	Indels 0;	Gaps 0;
QY	1	MWLQNLLLGLGTVVYSPAPRQPSVPTRPQHWDAIKEALSLNNSSDTAAINNEIVVV	60		
Db	1	MWLQNLLLGLGTVVCSAPRQPSVPTRPQHWDAIKEALSLNDSDDTAAVNDIVVV	60		
QY	61	SETFDAAEELTCLQRLKLYKQGRGSLIKLEGPLTMMASHYKHCPTTETSCATQMITF	120		
Db	61	SEMFDSQEPFCLQRLKLYKQGRGSLTSLTGSITMMASHYKHCPTTQETSCETQIIIF	120		
QY	121	KSPKKNLKDPLFPIFPDCWKPAQK	144		
Db	121	KSPKENLKDPLFIIPDCWEPVOK	144		

```

; APPLICANT: Dede, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 69622
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Cervus elaphus
US-09-791-537-69622

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[illegible]

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RESUL1: 8
US-11-301-800-15
; Sequence 15, Application US/11301800
; GENERAL INFORMATION:
; APPLICANT: BUELOW, ROLAND
; APPLICANT: PLATZER, JOSEF
; TITLE OF INVENTION: IMPROVED DNA IMMUNIZATION WITH
; TITLE OF INVENTION: RECOMBINASE/TRANSPOBASE
; FILE REFERENCE: 39691-0013
; CURRENT APPLICATION NUMBER: US/11/301,800
; CURRENT FILING DATE: 2005-12-12
; PRIOR APPLICATION NUMBER: US 60/636,361
; PRIOR FILING DATE: 2004-12-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Cervus
US-11-301-800-15

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	Query Match	83.4%	Score 633;	DB 43;	Length 144;
	Best Local Similarity	84.0%;	Pred. No. 8.9e-63;		
	Matches 121;	Conservative 7;	Mismatches 16;	Indels 0;	Gaps 0;
Qy	1 MWLQNLLLLGTVVYSMAPTRPSPVTPRPQHVDAIKEALLNNSSDAAIINNETVEVV	60			
Dd	1 MWLQNLLLLGTVVCSFSAPTBPASVPTRPQHVDAIKEALLNNSSDAAIINNETVEVV	60			
Qy	61 SETFFDABELTCLQRLKLYKGRLSGLIKLEGPLTMWASHYQHCPTPTLETSCATQMIF	120			
Dd	61 SEFPDSQEPCLOTRLKLYKGRLSGLISLSGSLTMWARHYEQHCPTQTSETQTITF	120			
Qy	121 KSPKKNLKDLFEIPFDCCWKPAQK	144			
Dd	121 KSPKENLKDFLIIPFDCCWEPAQK	144			

```
RESULT 9
US-09-791-82598
; Sequence 82598, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82598
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-791-82598

Query Match      78.7%; Score 597; DB 27; Length 144;
Best Local Similarity 77.1%; Pred. No. 1.1e-58;
Matches 111; Conservative 14; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLLLLGTVVYVSMPTPTQPSVTPRWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQNLLLLGTVVCSISAPTRPPSPVTPRWQHVDAIKEALSLNNSSDTAAVMNETVDIV 60
QY 61 SETFDAEELTCLOTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 CEMFDPQPTCVQTRNLNLYKQGLRSLRLKSPLLAKHYEQHCPLETSCETQSIITF 120
QY 121 KSFKKNLKDFLFEIPDFDCWKPAK 144
DB 121 KSFKDSLKNKFLFTIPDFDCWEPAK 144

RESULT 10
US-09-791-537-101680
; Sequence 101680, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 101680
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-791-537-101680

Query Match      77.3%; Score 587; DB 27; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.5e-57;
Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 MWLQNLLLLGTVVYVSMPTPTQPSVTPRWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQNLLLLGTVVCSISAPTRPPSPVTPRWQHVDAIKEALSLNNSSDTAAVMNETVDIV 60
QY 61 SETFDAEELTCLOTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 CEMFDPQPTCVQTRNLNLYKQGLRSLRLKSPLLAKHYEQHCPLETSCETQSIITF 120
QY 121 KSFKKNLKDFLFEIPDFDCWKPAK 144
DB 121 KSFKDSLKNKFLFTIPDFDCWEPAK 144
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RESULT 11
US-11-301-800-12
; Sequence 12, Application US/11301800
; GENERAL INFORMATION:
; APPLICANT: BUELOW, ROLAND
; APPLICANT: PLATZER, JOSEF
; TITLE OF INVENTION: IMPROVED DNA IMMUNIZATION WITH
; TITLE OF INVENTION: RECOMBINASE/TRANSPPOSASE
; FILE REFERENCE: 39691-0013
; CURRENT APPLICATION NUMBER: US/11/301,800
; CURRENT FILING DATE: 2005-12-12
; PRIOR APPLICATION NUMBER: US 60/636,361
; PRIOR FILING DATE: 2004-12-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Sus
US-11-301-800-12

Query Match      77.3%; Score 587; DB 43; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.5e-57;
Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 MWLQNLLLLGTVVYVSMPTPTQPSVTPRWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQNLLLLGTVVCSISAPTRPPSPVTPRWQHVDAIKEALSLNNSSDTAAVMNETVDIV 60
QY 61 SETFDAEELTCLOTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 CEMFDPQPTCVQTRNLNLYKQGLRSLRLKSPLLAKHYEQHCPLETSCETQSIITF 120
QY 121 KSFKKNLKDFLFEIPDFDCWKPAK 144
DB 121 KSFKDSLKNKFLFTIPDFDCWGPVK 144

RESULT 12
PCT-US00-06067-114
; Sequence 114, Application PC/TUS0006067
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAL1 LIGAND
; FILE REFERENCE: 99-16PC
; CURRENT APPLICATION NUMBER: PCT/US00/06067
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 09/264,908
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 09/265,992
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-06067-114

Query Match      77.2%; Score 586; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.9e-57;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLLLLGTVVYVSMPTPTQPSVTPRWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQNLLLLGTVVCSISAPTRPPSPVTPRWQHVDAIQARRLLNLSRDTAAEMNETVEV 60
QY 61 SETFDAEELTCLOTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
```

Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 13
PCT-US02-32263-18
; Sequence 18, Application PC/TUS0232263
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Howe, Carlyn
; APPLICANT: Bakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
; FILE REFERENCE: 040853-01-5050WO
; CURRENT APPLICATION NUMBER: PCT/US02/32263
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/334,233
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 18
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-32263-18

Query Match 77.2%; Score 586; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.9e-57;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
QY 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAAMNETVEV 60
Db 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 14
PCT-US02-34502-10
; Sequence 10, Application PC/TUS0234502
; GENERAL INFORMATION:
; APPLICANT: ZymoGenetics, Inc.
; TITLE OF INVENTION: ZALPHA11 LIGAND ANTAGONISTS
; FILE REFERENCE: 01-37PC
; CURRENT APPLICATION NUMBER: PCT/US02/34502

; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/337,586
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-34502-10

Query Match 77.2%; Score 586; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.9e-57;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
QY 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAAMNETVEV 60
Db 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 15
PCT-US02-40891-447
; Sequence 447, Application PC/TUS0240891
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PFS64PCT
; CURRENT APPLICATION NUMBER: PCT/US02/40891
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: 60/423,623
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/351,360
; PRIOR FILING DATE: 2002-01-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 447
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-40891-447

Query Match 77.2%; Score 586; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.9e-57;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
QY 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAAMNETVEV 60
Db 1 MWLQNLILLGTVVYMPAPTRQPSVTPRQWHDVDAIKALSLLNNSDSTAAMNETVEV 60


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Db 61 SEMFDLQPTCLQRLKLYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
Qy 121 KSFKNLKDFLFPIPPDCWKPAQK 144
:|||||:|||||:|||||:
Db 121 ESFKNLKDFLLVIPDCWEPVQE 144

RESULT 2
US-11-429-373-448
; Sequence 448, Application US/11429373
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,373
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 448
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-373-448

Query Match 77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.2e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLTGVVYGNPAPTRQSPVTRPQHVDAIKEALSLNNSDPTAAIMNETVEV 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MWLQNLGLLTGVVYGNPAPTRQSPVTRPQHVDAIKEALSLNNSDPTAAIMNETVEV 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SETFDAELTCLQRLKLYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SEMFDLQPTCLQRLKLYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 KSFKNLKDFLFPIPPDCWKPAQK 144
:|||||:|||||:|||||:
Db 121 ESFKNLKDFLLVIPDCWEPVQE 144

RESULT 3
US-11-429-373-540
; Sequence 540, Application US/11429373
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,373
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
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; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 540
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-373-540

Query Match 77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.2e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLTGVVYGNPAPTRQSPVTRPQHVDAIKEALSLNNSDPTAAIMNETVEV 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MWLQNLGLLTGVVYGNPAPTRQSPVTRPQHVDAIKEALSLNNSDPTAAIMNETVEV 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 SETFDAELTCLQRLKLYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SEMFDLQPTCLQRLKLYKQGLRSLTKLKGPLTMASHYKQHCPTPTSCATQIITF 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 KSFKNLKDFLFPIPPDCWKPAQK 144
:|||||:|||||:|||||:
Db 121 ESFKNLKDFLLVIPDCWEPVQE 144

RESULT 4
US-11-429-373-541
; Sequence 541, Application US/11429373
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,373
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
```



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; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 541
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-373-541

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	Query Match	77.2%	Score 586;	DB 7;	Length 144;
	Best Local Similarity	76.4%;	Pred. No. 1.2e-58;		
	Matches 110;	Conservative 15;	Mismatches 19;	Indels 0;	Gaps 0;
Qy	1	MWLNQLLLGLTVVYVYMPAPTRQPSVTRPQWHDVAIKEALLNSSDTAIKNMNETVEV	60		
Db	1	MWQSLLLGLTVACISISAPARSPSQPWEHVNAIQEARLLNLSRDTAAEMNETVEVI	60		
Qy	61	SETFDABELCLQTRLKLYKQGLRGSILKLEGLPTMMASHYKQHCPTLETSCATQITTF	120		
Db	61	SENFDLQETCLQTRLSELYKQGLRGSLTCLKGPLTMASHYKQHCPTTPEISCATQITTF	120		
Qy	121	KSPKKNLKFELFEPFDCWCPAQK	144		
Db	121	ESPKENLKDFLLVIPFDCWBPVQE	144		

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RESULT 5
US-11-429-374-447
; Sequence 447, Application US/11429374
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,374
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 447
; LENGTH: 144
; TYPE: PRT
; ORIGIN: Homo sapiens
US-11-429-374-447

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	Query Match	77.2%	Score 586;	DB 7;	Length 144;
	Best Local Similarity	76.4%;	Pred. No. 1.2e-58;		
	Matches 110;	Conservative	15;	Mismatches 19;	Indels 0; Gaps 0
QY	1	MWLQNLLLLGTVVYVYMPAPTRQPSPTRPWQVDAIKEALSLLNNSSTAAIMNTEVW	60		
Db	1	MWLQSLLLLTGACVSIAPAPSPSPQTPWPHVNAIQEARLLNLSRDTAAEMNTEVVI	60		
QY	61	SETFDABELCTLORLKLKYGKLRGSLIKLEBPLTMASHYKHQCHPPTLETSCATQMITF	120		

[illegible]

```

RESULT 6
US-11-429-374-448
; Sequence 448, Application US/11429374
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,374
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 448
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-374-448

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		Query Match	77.2%;	Score 586;	DB 7; Length 144;
		Best Local Similarity	76.4%;	Pred. No. 1.2e-58;	
Matches	110;	Conservative	15;	Mismatches 19;	Indels 0; Gaps 0;
Qy	1	MWLNQLLLGLTGTVVYSPMPAPTRQPSPVTFRPMQHVDVAIKEALSLNNSSDTAAMNETVEVV	60		
Dd	1	MWLQSLLLLGTGTVACISAPARSPSTQPWEHVNAIQEARRLNLNRDTAEAMNETVEVI	60		
Qy	61	SETFDAEELTCLQTLRKLKYGQRGSILIKUEGPLTWMAASHYKHCPPTLETSCATOMITTF	120		
Dd	61	SEMFEDLQEFPCTQLRLLELYKQGLRGSLTKLKGPITWMASHYKHCHPPTPEISCATQIITFF	120		
Qy	121	KSPKNLKKOFLFEIPFDCKWPQAOK	144		
Dd	121	ESEKENLKDPLLVIPDCEMPPVOE	144		

```

RESULT 7
US-11-429-374-540
; Sequence 540, Application US/11429374
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429, 374
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204

```



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QY 61 SETFDAEELTCLQRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
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Db 61 SEMFDLQPTCLQRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KSFKNLKDPLFEIPFDCWKPAQK 144
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ESFKENLKDPLLVIPFDCWEPVQE 144
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 10

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US-11-429-276-448
; Sequence 448, Application US/11429276
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 540
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-540
```

```
Query Match 77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.2e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILLGTVVYVSMPTPTQSPVTPWQHVDAIKEALSLNNSSDTAATMNETVEVV 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MWLQNLILLGTVVYVSMPTPTQSPVTPWQHVDAIKEALSLNNSSDTAATMNETVEVI 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SETFDAEELTCLQRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SEMFDLQPTCLQRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KSFKNLKDPLFEIPFDCWKPAQK 144
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ESFKENLKDPLLVIPFDCWEPVQE 144
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
US-11-429-276-448
Query Match 77.2%; Score 586; DB 7; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.2e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;
```

```
QY 1 MWLQNLILLGTVVYVSMPTPTQSPVTPWQHVDAIKEALSLNNSSDTAATMNETVEVV 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MWLQNLILLGTVVYVSMPTPTQSPVTPWQHVDAIKEALSLNNSSDTAATMNETVEVI 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SETFDAEELTCLQRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SEMFDLQPTCLQRLKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMTTF 120
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 KSFKNLKDPLFEIPFDCWKPAQK 144
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 ESFKENLKDPLLVIPFDCWEPVQE 144
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 11

```
US-11-429-276-540
; Sequence 540, Application US/11429276
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
```

```
US-11-429-276-541
; Sequence 541, Application US/11429276
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
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; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 541
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-541

Query Match
Best Local Similarity 77.2%; Score 586; DB 7; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLILLGTGVVSMPTPTQPSVTRPQHWDAIKELSLNNSSDTAAIMNETVEV 60
Db 1 MWLQNLILLGTGVVSMPTPTQPSVTRPQHWDAIKELSLNNSSDTAAIMNETVEV 60

Qy 61 SHTFDAELTCLQTRKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQITF 120
Db 61 SHMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMMASHYKQHCPTLETSCATQITF 120

Qy 121 KSFKNLKDFLFEIPDFCQKPAQK 144
Db 121 ESFKENLKDFLLVIPDFCWEVQEQ 144

RESULT 13
US-11-429-373-324
; Sequence 324, Application US/11429373
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,373
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 324
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-374-324

Query Match
Best Local Similarity 77.2%; Score 586; DB 7; Length 729;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

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Db 1 MWLQNLILLGTGVVSMPTPTQPSVTRPQHWDAIKELSLNNSSDTAAIMNETVEV 60

Qy 61 SHTFDAELTCLQTRKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQITF 120
Db 61 SHMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMMASHYKQHCPTLETSCATQITF 120

Qy 121 KSFKNLKDFLFEIPDFCQKPAQK 144
Db 121 ESFKENLKDFLLVIPDFCWEVQEQ 144

RESULT 14
US-11-429-374-324
; Sequence 324, Application US/11429374
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,374
; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 324
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-374-324

Query Match
Best Local Similarity 77.2%; Score 586; DB 7; Length 729;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLILLGTGVVSMPTPTQPSVTRPQHWDAIKELSLNNSSDTAAIMNETVEV 60
Db 1 MWLQNLILLGTGVVSMPTPTQPSVTRPQHWDAIKELSLNNSSDTAAIMNETVEV 60

Qy 61 SHTFDAELTCLQTRKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQITF 120
Db 61 SEMFDLQEPCTCLQTRLELYKQGLRSLTKLKGPLTMMASHYKQHCPTLETSCATQITF 120

Qy 121 KSFKNLKDFLFEIPDFCQKPAQK 144
Db 121 ESFKENLKDFLLVIPDFCWEVQEQ 144

RESULT 15
US-11-429-276-324
; Sequence 324, Application US/11429276
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Albumin Fusion Proteins
; FILE REFERENCE: PF564
; CURRENT APPLICATION NUMBER: US/11/429,276
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; CURRENT FILING DATE: 2006-05-08
; PRIOR APPLICATION NUMBER: 10/775,204
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: PCT/US02/40891
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/341,811
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/360,000
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/378,950
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/398,008
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/411,355
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/414,984
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/417,611
; PRIOR FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/420,246
; PRIOR FILING DATE: 2002-10-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2222
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 324
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-429-276-324

Query Match      77.2%; Score 586; DB 7; Length 729;
Best Local Similarity 76.4%; Pred. No. 1.1e-57;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy      1 MWLQNLGLGTVVYSPAPTRQSPVTRPWQHVDAIKEALSLNNSSDTAAIMNETVEVV 60
Db      1 MWLQSLLLGLTVACSIAPARSPSPSTQPEHVNAIQEARRLLNLSRDTAAEMNETVEVI 60

Qy      61 SETPDABELTCLQTRLKLYKQGLRGLSLKLEGLTMMASHYKQHCPTTLETSCATQMITF 120
Db      61 SEMFDLQEPFTCLQTRLELYKQGLRGLSLTKLKGPLTMMASHYKQHCPTTLETSCATQITTF 120

Qy      121 KSFKKNLKDPLFEIPFDCWKPAQK 144
Db      121 ESFKENLKDPLVIPPDCWEPVQOE 144

Search completed: May 25, 2006, 15:13:02
Job time : 19 secs
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 00:41:25 ; Search time 3045 Seconds
(without alignments)
9135.346 Million cell updates/sec

Title: US-10-614-481-8
Perfect score: 435
Sequence: 1 atgtggctgcagaacctgtct.....ggaagccagccagaagtaa 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
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2: gb_pat.*
3: gb_ph.*
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5: gb_pr.*
6: gb_ro.*
7: gb_sts.*
8: gb_sy.*
9: gb_un.*
10: gb_vl.*
11: gb_ov.*
12: gb_hcg.*
13: gb_in.*
14: gb_on.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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2	435	100.0	435	2 AX057390	AX057390 Sequence
3	435	100.0	435	2 AX067832	AX067832 Sequence
4	432	99.3	438	14 AF448481	AF448481 Equus cab
5	419.8	96.5	779	14 AY040203	AY040203 Equus cab
6	363.2	83.5	432	14 O06MCSF	X55991 Ovine GM-CS
7	363	83.4	435	14 D0010419	D0010419 Capra hir
8	363	83.4	495	14 O06MCSFR	X53561 Ovine mRNA
9	358.4	82.4	432	14 CFU14392	U14392 Cervus elap
10	334.2	76.8	435	14 P1GGMCSF	D21074 Sus scrofa
11	332.6	76.5	435	2 AX067831	AX067831 Sequence
12	332.6	76.5	435	14 SSU67175	U67175 Sus scrofa
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c 16	332.6	76.5	444	2 AR241566	AR241566 Sequence
17	332.6	76.5	444	2 AR254521	AR254521 Sequence
c 18	332.6	76.5	444	2 AR254522	AR254522 Sequence

19	332.6	76.5	798	2 AR028919	AR028919 Sequence
20	332.6	76.5	798	2 AR031114	AR031114 Sequence
21	332.6	76.5	798	2 I33052	I33052 Sequence 10
22	332.6	76.5	830	14 AV116504	AV116504 Sus scrofa
23	331.6	76.2	435	2 CQ834914	CQ834914 Sequence
24	331.2	76.1	432	2 AR302748	AR302748 Sequence
25	331.2	76.1	432	2 AR696282	AR696282 Sequence
26	331.2	76.1	432	2 AX078785	AX078785 Sequence
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29	331	76.1	435	2 AR533388	AR533388 Sequence
30	331	76.1	435	2 AX067830	AX067830 Sequence
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32	331	76.1	756	2 CQ721607	CQ721607 Sequence
33	331	76.1	756	2 CQ803372	CQ803372 Sequence
34	331	76.1	763	2 E02287	E02287 DNA encodin
35	331	76.1	781	2 CS032694	CS032694 Sequence
36	331	76.1	781	2 CS035823	CS035823 Sequence
37	331	76.1	781	2 CS041646	CS041646 Sequence
38	331	76.1	781	2 CS044775	CS044775 Sequence
39	331	76.1	781	2 CS195784	CS195784 Sequence
40	331	76.1	787	2 I08093	I08093 Sequence 1
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42	331	76.1	787	2 I08401	I08401 Sequence 1
43	331	76.1	787	2 I09140	I09140 Sequence 1
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ALIGNMENTS

RESULT 1
AR429724
LOCUS AR429724 435 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6645740.
ACCESSION AR429724
VERSION AR429724.1 GI:40190061
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 435)
AUTHORS Bublout,M., Perez,J.M. and Andreoni,C.M.P.
TITLE Nucleic acids encodings equine GM-CSF
JOURNAL Patent: US 6645740-A 8 11-NOV-2003;
Merical Limited and Merical LLC; London;
GBX;
FEATURES
source Location/Qualifiers
1..435
/organism="unknown"
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Qy	1	ATGTGGCTGCAGAACTGCTTCTCTGGCACTGTGTTTACAGCATGCCGCCACC	60			
Db	1	ATGTGGCTGCAGAACTGCTTCTCTGGCACTGTGTTTACAGCATGCCGCCACC	60			
Qy	61	CGCCAAACCCAGCCCTGTCACTCGGCCCTGdCAGCATGTGGATGCCATCAAGGAGGCCCTG	120			
Db	61	CGCCAAACCCAGCCCTGTCACTCGGCCCTGdCAGCATGTGGATGCCATCAAGGAGGCCCTG	120			
Qy	121	AGCCTTCTTGAAACAAACAGTAGTGACACTGCTGTATCATGAATGAAACAGTAGTCGTC	180			
Db	121	AGCCTTCTTGAAACAAACAGTAGTGACACTGCTGTATCATGAATGAAACAGTAGTCGTC	180			
Qy	181	TCTGAAAGCTTTGACGCGAGGAGCTGACATGCCCTGCGACTCGCTGAAGCTGTACAA	240			
Db	181	TCTGAAAGCTTTGACGCGAGGAGCTGACATGCCCTGCGACTCGCTGAAGCTGTACAA	240			

241 CAGGCTTTCGGGGCAGGCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300
Db CAGGCTTTCGGGGCAGGCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300
301 TACAAGCAGCACTGCCCGCCACCTCGAAGCTTCTCTGTGCAACCCAGATGATCACTTC 360
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361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCTTTGACTGCTGGAAG 420
Db AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCTTTGACTGCTGGAAG 420
421 CCAGCCCAAGAGTAA 435
Db CCAGCCCAAGAGTAA 435
RESULT 2
AX057390 435 bp DNA linear PAT 17-JAN-2001
LOCUS Sequence 8 from Patent WO0077210.
DEFINITION AX057390
ACCESSION AX057390
VERSION AX057390.1 GI:12310131
KEYWORDS Equus sp.
SOURCE Equus sp.
ORGANISM Equus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
1
Bublot,M., Perez,J.M. and Andreoni,C.M.
Fischer,L.J., barzu-le Roux,S. and Audonnet,J.C.
Dna vaccines for pets and sport animals
Patent: WO 0077210-A 8 21-DEC-2000;
Merial (FR)
FEATURES
source Location/Qualifiers
1 . 435
/organism="Equus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:46122"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9e-105;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
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121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTACAAA 180
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181 TCTGAAACGTTTGACCGCGAGGAGCTGACATGCCCTGCAGACTCGGCTGAAGCTGTACAAA 240
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Db 301 TACAAGCAGCACTGCCCGCCACCTCGAAGCTTCTCTGTGCAACCCAGATGATCACTTC 360
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Qy 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCTTTGACTGCTGGAAG 420
Db 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCTTTGACTGCTGGAAG 420
421 CCAGCCCAAGAGTAA 435
Qy 421 CCAGCCCAAGAGTAA 435
Db 421 CCAGCCCAAGAGTAA 435
RESULT 4
AF448481 438 bp mRNA linear MAM 12-AUG-2002
LOCUS Equus caballus granulocyte-macrophage colony-stimulating factor
DEFINITION (GM-CSF) mRNA, partial cds.
ACCESSION AF448481
VERSION AF448481.2 GI:22208937
KEYWORDS

421 CCAGCCCAAGAGTAA 435
Db 421 CCAGCCCAAGAGTAA 435
RESULT 3
AX067832 435 bp DNA linear PAT 19-JAN-2001
LOCUS Sequence 69 from Patent WO0077043.
DEFINITION AX067832
ACCESSION AX067832
VERSION AX067832.1 GI:12329710
KEYWORDS Equus sp.
SOURCE Equus sp.
ORGANISM Equus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
1
Fischer,L.J., barzu-le Roux,S. and Audonnet,J.C.
Dna vaccines for pets and sport animals
Patent: WO 0077043-A 69 21-DEC-2000;
Merial (FR)
FEATURES
source Location/Qualifiers
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/organism="Equus sp."
/mol_type="unassigned DNA"
/db_xref="taxon:46122"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9e-105;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
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61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
Qy 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
Db 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTACAAA 180
Qy 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTACAAA 180
Db 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGTACAAA 180
181 TCTGAAACGTTTGACCGCGAGGAGCTGACATGCCCTGCAGACTCGGCTGAAGCTGTACAAA 240
Qy 181 TCTGAAACGTTTGACCGCGAGGAGCTGACATGCCCTGCAGACTCGGCTGAAGCTGTACAAA 240
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361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCTTTGACTGCTGGAAG 420
Qy 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCTTTGACTGCTGGAAG 420
Db 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCTTTGACTGCTGGAAG 420
421 CCAGCCCAAGAGTAA 435
Qy 421 CCAGCCCAAGAGTAA 435
Db 421 CCAGCCCAAGAGTAA 435
RESULT 4
AF448481 438 bp mRNA linear MAM 12-AUG-2002
LOCUS Equus caballus granulocyte-macrophage colony-stimulating factor
DEFINITION (GM-CSF) mRNA, partial cds.
ACCESSION AF448481
VERSION AF448481.2 GI:22208937
KEYWORDS

SOURCE	Equus caballus (horse)	Db	301	TACAAAGCAGCACTGCCCCCCCCACCTTCTGTGCAACCCAGATGATCACCTTC	360
ORGANISM	Equus caballus	Qy	361	AAAGCTTTCAAAAGCACTGAAGGATTTCTGTTTGAGATCCCGTTTCACTGCTGGAAG	420
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Db	361	AAAGCTTTCAAAAGCACTGAAGGATTTCTGTTTGAGATCCCGTTTCACTGCTGGAAG	420
AUTHORS	1 (bases 1 to 438)	Qy	421	CCAGCCCAAG 432	
TITLE	CDNA for equine GM-CSF	Db	421	CCAGCCCAAG 432	
REFERENCE	Unpublished				
AUTHORS	Vecchione, A., D'Mello, F., Kanellos, T.S., Howard, C.R., Hamblin, A.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2001) Department of Pathology and Infectious Diseases, Royal Veterinary College, Royal College Street, London NW1 0TU, UK				
REFERENCE	3 (bases 1 to 438)				
AUTHORS	Vecchione, A., D'Mello, F., Kanellos, T.S., Howard, C.R., Hamblin, A.S.				
TITLE	Direct Submission				
JOURNAL	Submitted (12-AUG-2002) Department of Pathology and Infectious Diseases, Royal Veterinary College, Royal College Street, London NW1 0TU, UK				
REMARK	Sequence update by submitter				
COMMENT	On Aug 12, 2002 this sequence version replaced gi:17646732.				
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source	1..438				
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	/db_xref="taxon:9796"				
gene	1..>438				
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CDS	1..>438				
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	/function="stimulates bone marrow progenitor cells to proliferate and differentiate"				
	/note="cytokine"				
	/codon_start=1				
	/product="granulocyte-macrophage colony-stimulating factor"				
	/protein_id="AAL41017.2"				
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	/translation="MWLQNLILLGTVVYVSMPTQPSVTPRQVHDAIKEALSLLN NSSDTAAMNETVEVSTFDAEULTCLQRLKLYKQGLRSLIKLEGLPTWASHYK QHCPTLETSCATQMITFKSPKKNLKDFLFEIPFCWNPRAKLE"				
ORIGIN					
Query Match	99.3%; Score 432; DB 14; Length 438;				
Best Local Similarity	100.0%; Pred. No. 5.6e-104;				
Matches 432; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				
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Db	1	ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGGTTTACAGCATGCCGCCACCCACC	60		
Qy	61	CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGAGCCCTG	120		
Db	61	CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGAGCCCTG	120		
Qy	121	AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACACAGTAGTAGTCTGTC	180		
Db	121	AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACACAGTAGTAGTCTGTC	180		
Qy	181	TCTGAAAGCTTTGACGCGAGAGCTGACATGCTTGGCAGACTCGCTGAAGCTGTACAA	240		
Db	181	TCTGAAAGCTTTGACGCGAGAGCTGACATGCTTGGCAGACTCGCTGAAGCTGTACAA	240		
Qy	241	CAGGCTTTCGCGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGCACCATGATGCCAGCCAC	300		
Db	241	CAGGCTTTCGCGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGCACCATGATGCCAGCCAC	300		
Qy	301	TACAAAGCAGCACTGCCCCCCCCACCTTCTGTGCAACCCAGATGATCACCTTC	360		

Db 61 CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120

Qy 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTCTATCATGAATGAAACAGTAGTAGTCTGTC 180

Db 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTCTATCATGAATGAAACAGTAGTAGTCTGTC 180

Qy 181 TCTGAAAGCTTTGAGCGCGAGAGCTGACATGCCCTGCGAGACTCGCCTGAAGCTGTACAAA 240

Db 181 TCTGAAAGCTTTGAGCGCGAGAGCTGACATGCCCTGCGAGACTCGCCTGAAGCTGTACAAA 240

Qy 241 CAGGCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCAGCCAC 300

Db 241 CAGGCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTTAAACCATGATGCCAGCCAC 300

Qy 301 TACAAGCAGCCTGCCCCCACCCTCGAAATCTCTGTGTGCAACCCAGCATGATCACCTTC 360

Db 301 TACAAGCAGCCTGCCCCCACCCTCGAAATCTCTGTGTGCAACCCAGCATGATCACCTTC 360

Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420

Db 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAA- 419

Qy 421 CCAGCCCAAGATA 435

Db 420 CCAGCCCAAGATA 434

RESULT 6

COGMCSE

LOCUS Ovine GM-CSF mRNA for granulocyte-macrophage colony stimulating factor. 432 bp mRNA linear MAM 18-APR-2005

DEFINITION

ACCESSION X55991

VERSION X55991.1 GI:6983759

KEYWORDS cytokine; granulocyte-macrophage colony stimulating factor.

SOURCE Ovis aries (sheep)

ORGANISM Ovis aries

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.

REFERENCE 1

AUTHORS O'Brien, P.M., Rothel, J.S., Seow, H.F. and Wood, P.R.

TITLE Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stimulating factor (GM-CSF)

JOURNAL Immunol. Cell Biol. 69 (pt 1), 51-55 (1991)

PUBMED 1869289

REFERENCE 2 (bases 1 to 432)

AUTHORS O'Brien, P.

TITLE Direct Submission

JOURNAL Submitted (12-OCT-1990) O'Brien P., Commonwealth Scientific & Industrial Research, (CSIRO) Division of Animal Health, Private Bag No 1, Parkville Vic 3052, Australia

COMMENT Stimulates bone marrow progenitor cells to proliferate and differentiate.

FEATURES

source Location/Qualifiers

1..432

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ORIGIN

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Best Local Similarity 90.0%; Pred. No. 1.2e-85;

Matches 389; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGACCCACCC 60

Db 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGACCCACT 60

Qy 61 CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120

Db 61 CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120

Qy 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTCTATCATGAATGAAACAGTAGTAGTCTGTC 180

Db 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTCTATCATGAATGAAACAGTAGTAGTCTGTC 180

Qy 181 TCTGAAAGCTTTGAGCGCGAGAGCTGACATGCCCTGCGAGACTCGCCTGAAGCTGTACAAA 240

Db 181 TCTGAAAGCTTTGAGCGCGAGAGCTGACATGCCCTGCGAGACTCGCCTGAAGCTGTACAA 240

Qy 241 CAGGCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCAGCCAC 300

Db 241 CAGGCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCAGCCAC 300

Qy 301 TACAAGCAGCCTGCCCCCACCCTCGAAATCTCTGTGTGCAACCCAGCATGATCACCTTC 360

Db 301 TACAAGAAACACTGCCCCCACCCTCGAAGAACTTCTGTGAAACCCAGATTATCACCTTC 360

Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420

Db 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTTATTCATTCCTTTGACTGCTGGAA 420

Qy 421 CCAGCCCAAGATA 432

Db 421 CCAGCCCAAGATA 432

RESULT 7

LOCUS DQ010419

DEFINITION Capra hircus granulocyte-macrophage colony stimulating factor (GM-CSF) mRNA, complete cds.

ACCESSION DQ010419

VERSION DQ010419.1 GI:62825817

KEYWORDS

SOURCE Capra hircus (goat)

ORGANISM Capra hircus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Capra.

REFERENCE 1 (bases 1 to 435)

AUTHORS Shu, D.Q., Cao, S.X., Mao, D.G., Wu, Z.M. and Yang, L.G.

TITLE Cloning and Sequence Analysis of Capra Hircus Granulocyte-macrophage Colony Stimulating Factor (GM-CSF)

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 435)

AUTHORS Shu, D.Q., Cao, S.X., Mao, D.G., Wu, Z.M. and Yang, L.G.

TITLE Direct Submission

JOURNAL Submitted (18-APR-2005) The Animal Breed Institute, Nanjing Agricultural University, Nanjing, Jiangsu 210095, China

FEATURES

source Location/Qualifiers

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ORIGIN

Query Match 83.4%; Score 363; DB 14; Length 435;
Best Local Similarity 89.7%; Pred. No. 1.3e-85;
Matches 390; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGGTTTACAGCATGCCACCCACC 60
DB 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGGTTTACAGCATGCCACCCACT 60
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QY 421 CCAGCCCAAGAGTAA 435
DB 421 CCAGTCCAGAGTAA 435

RESULT 8
OOGMCSFR 495 bp mRNA linear MAM 18-APR-2005
LOCUS
DEFINITION
Ovine mRNA for granulate-macrophage stimulating factor (GM-CSF).
X53561
VERSION
X53561.1 GI:1800
KEYWORDS
granulocyte-macrophage colony stimulating factor; signal peptide.
SOURCE
Ovis aries (sheep)
ORGANISM
Ovis aries

REFERENCE
1
McInnes, C.J. and Haig, D.M.
AUTHORS
Cloning and expression of a cDNA encoding ovine
TITLE
granulocyte-macrophage colony-stimulating factor
JOURNAL
Gene 105 (2), 275-279 (1991)
PUBMED
1937025
REFERENCE
2 (bases 1 to 495)
McInnes, C.J.
AUTHORS
Direct Submision
TITLE
Submitted (20-JUN-1990) McInnes C.J., Moredun Research Institute,
JOURNAL
408 Gilmerton Rd., Edinburgh EH17 7JH, Scotland, UK
LOCATION/Qualifiers
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ORIGIN

Query Match 83.4%; Score 363; DB 14; Length 495;
Best Local Similarity 89.7%; Pred. No. 1.4e-85;
Matches 390; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
QY 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGGTTTACAGCATGCCACCCACC 60
DB 14 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGGTTTACAGCATGCCACCCACT 73
QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
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QY 121 AGCCTTCTGAACCAACAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
DB 121 AGCCTTCTGAACCAACAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
QY 181 TCTGAAAGCTTTGACGCGAGGAGCTGACATGCCGTCAGACTCGCTGAAGCTGTACAAA 240
DB 181 TCTGAAAGCTTTGACGCGAGGAGCTGACATGCCGTCAGACTCGCTGAAGCTGTACAAA 240
QY 241 CAGGCTTTCGCGGGCAGGCTCATCAAGCTGGAAGGCCCTTGACCATGATGCCAGCCAC 300
DB 241 CAGGCTTTCGCGGGCAGGCTCATCAAGCTGGAAGGCCCTTGACCATGATGCCAGCCAC 300
QY 301 TACAAGCAGACTGCCCCCACCCTCGAAGCTTCTGTTTGAGATCCCTTTGACTGCTGGAG 360
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DB 361 AAAAGTTTCAAAAGAACTGAAGATTTCTGTTTGAGATCCCTTTGACTGCTGGAG 420
QY 421 CCAGCCCAAGAGTAA 435
DB 421 CCAGTCCAGAGTAA 448

RESULT 9
CEU14392 432 bp mRNA linear MAM 14-SEP-1994
LOCUS
DEFINITION
Cervus elaphus granulocyte-macrophage colony-stimulating factor
U14392
VERSION
U14392.1 GI:537895
KEYWORDS
Cervus elaphus (red deer)
SOURCE
Cervus elaphus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Cervidae; Cervinae; Cervus.
REFERENCE
1 (bases 1 to 432)
Lockhart, E.A.
AUTHORS

TITLE Cloning and sequencing of cervine GM-CSF
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 432)
AUTHORS Lockhart, E.A.
TITLE Direct Submission
JOURNAL Submitted (05-SEP-1994) Euan A Lockhart, Microbiology, Deer Research Laboratory, University of Otago, Union St., Dunedin, New Zealand

FEATURES
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/gene="GM-CSF"
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ORIGIN
Query Match 82.4%; Score 358.4; DB 14; Length 432;
Best Local Similarity 89.4%; Pred. No. 2.2e-84;
Matches 386; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
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QY 61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DDB 61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTATCATGAATGAACAGTAGTGAAGTCGTC 180
DDB 121 AGCCTTCTGAACAACAGTAGTGACACTGCTATCATGAATGAACAGTAGTGAAGTCGTC 180
QY 181 TCTGAAACCTTTGACGCGCAGAGCTGACATGCCCTGCAGACTCGGCTGAAAGCTGTACAAA 240
DDB 181 TCTGAAATGTTTGATCCAGAGCCGACATGCCCTGCAGACTCGGCTGAAAGCTGTACAAA 240
QY 241 CAGGCTTTGCGGGCAGCCTCATCAAGCTCGAAGCCCTTGAACCATGATGCCAGCCAC 300
DDB 241 CAGGCTTTGCGGGCAGCCTCATCAAGCTCGAAGCCCTTGAACCATGATGCCAGCCAC 300
QY 301 TACAGAGCACTGCCCCCACCCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
DDB 301 TACAGAGCACTGCCCCCACCCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGAGATCCCGTTTGACTGTCTGGAAG 420
DDB 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGAGATCCCGTTTGACTGTCTGGAAG 420
QY 421 CCAGCCCAAG 432
DDB 421 CCAGCCCAAG 432

RESULT 10
PIGGMCSF
LOCUS
DEFINITION Sus scrofa GM-CSF mRNA for granulocyte-macrophage colony-stimulating factor, complete cds.
435 bp mRNA linear MAM 11-JAN-2003

ACCESSION D21074
VERSION D21074.1 GI:497829
KEYWORDS Sus scrofa (pig)
SOURCE Sus scrofa
ORGANISM Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 Inumaru, S. and Takamatsu, H.
AUTHORS cDNA cloning of porcine granulocyte-macrophage colony-stimulating factor
TITLE Immunol. Cell Biol. 73 (5), 474-476 (1995)
JOURNAL 8595928
PUBMED 2 (bases 1 to 435)
REFERENCE Inumaru, S.
AUTHORS Direct Submission
TITLE Submitted (06-OCT-1993) Shigeki Inumaru, National Institute of Animal Health, Biological Products Research Division; 3-1-1, Kannondai, Tsukuba, Ibaraki 305, Japan (Tel:81-298-38-8624, Fax:81-298-38-7880)
JOURNAL Location/Qualifiers
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/inference="non-experimental evidence, no additional details recorded"
/note="GM-CSF"
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/protein_id="BAA04649.1"
/db_xref="GI:497830"
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/inference="non-experimental evidence, no additional details recorded"
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Query Match 76.8%; Score 334.2; DB 14; Length 435;
Best Local Similarity 85.5%; Pred. No. 6.1e-78;
Matches 372; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60
DDB 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60
QY 61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DDB 61 CGCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTATCATGAATGAACAGTAGTGAAGTCGTC 180
DDB 121 AGCCTTCTGAACAACAGTAGTGACACTGCTATCATGAATGAACAGTAGTGAAGTCGTC 180
QY 181 TCTGAAACCTTTGACGCGCAGAGCTGACATGCCCTGCAGACTCGGCTGAAAGCTGTACAAA 240
DDB 181 TGTGAAATGTTTGATCCAGAGCCGACATGCCCTGCAGACTCGGCTGAAAGCTGTACAA 240
QY 241 CAGGCTTTGCGGGCAGCCTCATCAAGCTCGAAGCCCTTGAACCATGATGCCAGCCAC 300
DDB 241 CAGGCTTTGCGGGCAGCCTCATCAAGCTCGAAGCCCTTGAACCATGATGCCAGCCAC 300
QY 301 TACAGAGCACTGCCCCCACCCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
DDB 301 TATGAGAGCACTGCCCCCTCACCGAGGAACCTTCTGTGAAACCCAGTCTATCACCTTC 360
QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGAGATCCCGTTTGACTGTCTGGAAG 420

Db	361	AAAAGTTTCAAGACAGTCTGAACAAATTTCTTTTACCATCCCCCTTGACTGCTGGGAA	420
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Db	421	CCAGCCCAAGAGTGA	435
RESULT 11			
AX067831			
LOCUS	AX067831	435 bp	DNA linear PAT 19-JAN-2001
DEFINITION	Sequence 68 from Patent WO077043.		
ACCESSION	AX067831		
VERSION	AX067831.1	GI:12329709	
KEYWORDS	Felis.catus (cat)		
SOURCE	Felis catus		
ORGANISM	Felis catus		
REFERENCE			
AUTHORS	Fischer,L.J., barzu-le Roux,S. and Audonnet,J.C.		
TITLE	Dna vaccines for pets and sport animals		
JOURNAL	Patent: WO 0077043-A 68 21-DEC-2000;		
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source	1..435		
Location/Qualifiers			
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Query Match	76.5%;	Score 332.6;	DB 2; Length 435;
Best Local Similarity	85.3%;	Pred. No. 1.6e-77;	
Matches 371;	Conservative 0;	Mismatches 64;	Indels 0; Gaps 0;
Qy	1	ATGTGGCTGCAGAACTGTTCTTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC	60
Db	1	ATGTGGCTGCAGAACTGTTCTTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC	60
Qy	61	CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG	120
Db	61	AGTTCAACCCAGCTCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCTCTG	120
Qy	121	AGCCTTCTGAAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGTAGTCGTC	180
Db	121	AGCCTTCTGAAACAACAGTAGTGAATACTGTGTGATGAATGAGCAGTAGTAGTCGTC	180
Qy	181	TCTGAAACGTTTTCAGCCGAGGAGTGACATCCCTGCAGACTCGCCTGAAGCTGTACAAA	240
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Qy	241	CAGGCTTGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGAGCCAGCCAC	300
Db	241	CAGGCCCTACGGGGGAGCCTCATCAAGCTCGAAGGAGCCCTCTGAGGATGATGAGCCAA	300
Qy	301	TACAGCAGACTGCGCCGCCACCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTC	360
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Qy	361	AAAAGTTTCAAAAGAACTGAAGGATTTTCTGTGTGAGATCCCTTTGACTGCTGGAG	420
Db	361	AAAATTTTCAAAAGAACTCTGAAGGATTTTCTGTGTTTAAACATCCCTTTGACTGCTG	420
Qy	421	CCAGCCCAAGAGTAA	435
Db	421	CCAGTCAAGAGTGA	435
RESULT 12			
SSU67175			
LOCUS	SSU67175	435 bp	mRNA linear MAM 30-AUG-1996
DEFINITION	Sus scrofa granulocyte macrophage-colony stimulating factor (GM-CSF) mRNA, complete cds.		
ACCESSION	U67175		
VERSION	U67175.1	GI:1513327	
KEYWORDS	Sus scrofa (pig)		
SOURCE	Sus scrofa		
ORGANISM	Sus scrofa		
REFERENCE			
AUTHORS	Gloster,S.E., Sandeman,R.M. and Strom,A.D.G.		
TITLE	Cloning of a cDNA and gene encoding porcine granulocyte macrophage-colony stimulating factor (GM-CSF)		
JOURNAL	Unpublished		
AUTHORS	Gloster,S.E., Sandeman,R.M. and Strom,A.D.G.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-AUG-1996) Animal Health, CSIRO, Park Drive, Melbourne, VIC 3052, Australia		
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Best Local Similarity	85.3%;	Pred. No. 1.6e-77;	
Matches 371;	Conservative 0;	Mismatches 64;	Indels 0; Gaps 0;
Qy	1	ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC	60
Db	1	ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC	60
Qy	61	CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG	120
Db	61	CGCCCAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG	120
Qy	121	AGCCTTCTGAAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGTAGTCGTC	180
Db	121	AGCCTTCTTAACAACAGTAATGACACAGGGCTGTGATGAATGAACCCGATAGCTCGTC	180
Qy	181	TCTGAAACGTTTTCAGCCGAGGAGTGACATCCCTGCAGACTCGCCTGAAGCTGTACAAA	240
Db	181	TCTGAAATGTTTTCAGCCCTGAGGAGCGAAATGCCTGCAGACTCACCTAAAGCTGTACGAG	240
Qy	241	CAGGCTTGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGAGCCAGCCAC	300
Db	241	CAGGCCCTACGGGGGAGCCTCATCAAGCTCGAAGGAGCCCTCTGAGGATGATGAGCCAA	300
Qy	301	TACAGCAGACTGCGCCGCCACCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTC	360
Db	301	TACAGCAGACTGCGCCCTTACTTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC	360
Qy	361	AAAAGTTTCAAAAGAACTGAAGGATTTTCTGTGTGAGATCCCTTTGACTGCTGGAG	420
Db	361	AAAATTTTCAAAAGAACTCTGAAGGATTTTCTGTGTTTAAACATCCCTTTGACTGCTG	420
Qy	421	CCAGCCCAAGAGTAA	435
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RESULT 13
BD211587
LOCUS
DEFINITION
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION
BD211587
VERSION
BD211587.1 GI:33021357
KEYWORDS
JP 2002516104-A/93.
SOURCE
Felis catus (cat)
ORGANISM
Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
1 (bases 1 to 444)
Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
Patent: JP 2002516104-A 93 04-JUN-2002;
JOURNAL
HESKA CORP
OS Felis catus (cat)
PN JP 2002516104-A/93
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PT GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
PC A61K39/395,
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC C07K14/54,
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
G01N33/15,
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
Location/Qualifiers
FH Key Location/Qualifiers
FT CDS (10)..(441).

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Best Local Similarity 85.3%; Pred. No. 1.6e-77;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Db 310 TACAAGCAGACTGCCCCCTTACTCCGGAACCGCCTGTGAAACCCAGACTATCACCTTC 369
Qy 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
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Qy 421 CCAGCCCAAGAGTAA 435
Db 430 CCAGACCAGAGTAA 444

RESULT 14
BD211588/c
LOCUS
DEFINITION
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same.
ACCESSION
BD211588
VERSION
BD211588.1 GI:33021358
KEYWORDS
JP 2002516104-A/94.
SOURCE
Felis catus (cat)
ORGANISM
Felis catus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
Felinae; Felis.
1 (bases 1 to 444)
Sim,G., Yang,S., Dreitz,M.J. and Wonderling,R.S.
Canine and feline immunoregulatory proteins, nucleic acid molecules
and method of using the same
Patent: JP 2002516104-A 94 04-JUN-2002;
JOURNAL
HESKA CORP
OS Felis catus (cat)
PN JP 2002516104-A/94
PD 04-JUN-2002
PF 28-MAY-1999 JP 2000551002
PR 29-MAY-1998 US 60/087306
PT GEKKEE SIM,SHUMIN YANG,MATTHEW J DREITZ,RAMANI S WONDERLING PC
C12N15/09,A61K31/7088,A61K38/00,A61K38/21,A61K39/00,A61K39/395,
PC A61K39/395,
PC A61K45/00,A61K48/00,A61P37/02,A61P37/04,C07K14/475,C07K14/535,
PC C07K14/54,
PC C07K14/56,C07K14/705,C07K16/24,C07K16/28,C12N1/21,C12N5/10, PC
G01N33/15,
PC G01N33/50,C12N15/00,A61K37/02,A61K37/66,C12N5/00 CC Canine
and feline immunoregulatory proteins, nucleic acid CC
molecules and
CC method of using the same
Location/Qualifiers
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ORIGIN
Query Match 76.5%; Score 332.6; DB 2; Length 444;
Best Local Similarity 85.3%; Pred. No. 1.6e-77;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGTGTTTACAGATGCCGCCACCCACC 60
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Qy 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAAGTAGAGTCGTC 180
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Qy 421 CCAGCCCAAGAGTAA 435
Db 15 CCAGACCAGAGTAA 1

RESULT 15
AR241565
LOCUS AR241565 444 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 119 from patent US 6471957.
ACCESSION AR241565
VERSION AR241565.1 GI:27287274
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 444)
AUTHORS Sim,G.-K., Yang,S., Dreitz,M.J. and Wonderling,R.S.
TITLE Canine IL-4 immunoregulatory proteins and uses thereof
JOURNAL Patent: US 6471957-A 119 29-OCT-2002;
Heska Corporation; Fort Collins, CO;
EPX;

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ORIGIN

Query Match 76.5%; Score 332.6; DB 2; Length 444;
Best Local Similarity 85.3%; Pred. No. 1.6e-77;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGTGGTTTACAGCATGCCGACCCACC 60
Db 10 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACCTGTGGTTTACAGCATCTGACCCACC 69
Qy 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
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Qy 121 AGCCTTCTGAACAACAGTAGTAGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
Db 130 AGCCTTCTGAACAACAGTAGTAGAATAACTGTGTGATGAATGAAGCAGTAGAAGTCGTC 189
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Db 190 TCTGAATATGTTTGAACCTTGCAGGAGCGGAATGCCCTGCAGACTCACCTAAAGCTGTACGAG 249
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Qy 361 AAAAGCTTCAAAAAGAACCTGAAGGATTTCTGTTTGGATCCCGTTTGACTGCTGGAAG 420
Db 370 AAAAATTTCAAAGAGAACTCTGAAGGATTTCTGTTTAAACACCCCTTTGACTGCTGGGA 429
Qy 421 CCAGCCCAAGAGTAA 435
Db 430 CCAGACCAGAGTAA 444

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Job time : 3047 secs

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 00:33:29 ; Search time 449 Seconds
(without alignments)
6754.851 Million cell updates/sec

Title: US-10-614-481-8
Perfect score: 435
Sequence: 1 atgtggctgcagaactgtct.....ggaagccagccaggaagtaa 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_8.*

1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001as.*
5: Geneseq2001bs.*
6: Geneseq2002as.*
7: Geneseq2002bs.*
8: Geneseq2003as.*
9: Geneseq2003bs.*
10: Geneseq2003cs.*
11: Geneseq2003ds.*
12: Geneseq2004as.*
13: Geneseq2004bs.*
14: Geneseq2005s.*
15: Geneseq2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	4	ABZ80828 Equine gr
2	435	100.0	435	4	Aaf28953 Equine gr
3	363.2	83.5	432	2	Aaq24234 Ovine GM-
4	332.6	76.5	435	4	ABZ80827 Feline gr
5	332.6	76.5	444	3	Aaz55575 Feline GM
6	332.6	76.5	444	3	Aaz55576 Feline GM
7	332.6	76.5	798	2	Aaq64864 CHEF-2 ge
8	331.6	76.2	435	12	ADQ76022 Human GM-
9	331.6	76.2	435	15	Aef81846 Human GM-
10	331.2	76.1	432	4	Aaf55040 Nucleotid
11	331	76.1	435	2	AAV83189 Granulocy
12	331	76.1	435	3	Aaaf4392 DNA seque
13	331	76.1	435	4	ABZ80826 Feline gr
14	331	76.1	435	10	ACC78877 Human GM-
15	331	76.1	435	12	ADN49689 Human gra
16	331	76.1	435	13	ADU74365 Human gra
17	331	76.1	435	14	ADV42494 Human psy
18	331	76.1	435	14	ADY84979 Human Gra

19	331	76.1	435	14	ADY99885	AdY99885 Human imm
20	331	76.1	448	12	ADL16729	AdL16729 Human gra
21	331	76.1	763	2	AAQ04018	AAQ04018 Granulocy
22	331	76.1	781	12	ADN07714	ADN07714 Human G-C
23	331	76.1	781	12	ADP10387	ADP10387 Reference
24	331	76.1	781	14	ADY19523	ADY19523 DNA encod
25	331	76.1	781	14	ADY16394	ADY16394 DNA encod
26	331	76.1	781	14	ADZ26536	ADZ26536 Human GMS
27	331	76.1	781	14	ABE54678	ABE54678 DNA encod
28	331	76.1	787	1	AAH50364	AAH50364 Human gra
29	331	76.1	787	2	AAQ84865	AAQ84865 Clone pcd
30	331	76.1	789	3	AAA35017	AAA35017 Human ade
31	331	76.1	789	3	AAF21139	AAF21139 Human low
32	331	76.1	789	4	AAH28217	AAH28217 Nucleotid
33	331	76.1	789	10	ABZ96833	ABZ96833 Human nuc
34	331	76.1	789	11	ABD20682	ABD20682 Human pul
35	331	76.1	900	14	ADZ08738	ADZ08738 Adenovira
36	331	76.1	900	14	ABE95949	ABE95949 Oncolytic
37	331	76.1	900	15	AAE75748	AAE75748 Recombina
38	331	76.1	1172	14	ADZ08733	ADZ08733 Adenovira
39	331	76.1	1172	14	ABE95944	ABE95944 Oncolytic
40	331	76.1	1172	15	AAE75743	AAE75743 Recombina
41	331	76.1	5115	3	AAA35020	AAA35020 Human ade
42	331	76.1	5115	3	AAF21142	AAF21142 Human low
43	331	76.1	5115	10	ABZ96836	ABZ96836 Human nuc
44	331	76.1	5115	11	ABD20685	ABD20685 Human pul
45	331	76.1	7173	14	ADY99889	ADY99889 Exemplary

ALIGNMENTS

RESULT 1

ABZ80828
ID ABZ80828 standard; DNA; 435 BP.

XX AC ABZ80828;

XX DT 27-JUN-2003 (first entry)

XX DE Equine granulocyte-macrophage colony stimulating factor gene.

XX KW Granulocyte-macrophage colony stimulating factor; GM-CSF; ds; gene;

XX KW antibacterial; antiviral; vaccine; animal; immunogen; DMRIE;

XX KW cationic lipid; quaternary ammonium salt; canine distemper virus;

XX KW canine parainfluenza virus; canine herpes virus; feline herpes virus;

XX KW equine herpes virus; dog; cat; horse.

XX OS Equus caballus.

XX FH Key Location/Qualifiers

XX FT CDS 1..435

XX FT /*tag= a

XX FT /product= "Equine GM-CSF"

XX PN WO200077043-A2.

XX PD 21-DEC-2000.

XX PF 08-JUN-2000; 2000WO-FR001592.

XX PR 10-JUN-1999; 99FR-00007604.

XX PR 19-JUL-1999; 99US-0144490P.

XX (MERI-) MERIAL.

XX PA Fischer LJ, Barzu-Le Roux S, Audonnet JF;

XX PI WPI; 2001-071259/08.

XX DR P-PSDB; ABP98711.

XX DR DNA vaccine containing plasmid and cationic lipid containing quaternary ammonium salt, useful for protecting pets and sports animals against,

PT e.g. herpes virus.
XX
XX Example 10; Fig 26; 109pp; French.
XX
CC The invention relates to a novel DNA vaccine against pathogens that
CC affect pets and sports animals comprises a plasmid containing a sequence,
CC expressible in vivo, that encodes an immunogen from the relevant pathogen
CC and a cationic lipid containing a quaternary ammonium salt, particularly
CC N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium
CC (DMRIE). The immunogens are particularly taken from canine distemper
CC virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes
CC virus (CHV), feline herpes virus type 1 (FHV-1), equine herpes virus type
CC 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of
CC an immunogenic stimulation factor especially a granulocyte-macrophage
CC colony stimulation factor (GM-CSF) to enhance the immunogenic response.
CC The vaccines, which may be multivalent, are particularly used to protect
CC dogs, cats and horses against bacterial and viral diseases, particularly
CC those caused by the Paramyxoviridae. Formulations with the quaternary
CC ammonium salt provide a better immune response and thus more efficient
CC protection, particularly when administered subcutaneously. This sequence
CC represents the gene encoding an equine GM-CSF used in the invention
XX
SQ Sequence 435 BP; 109 A; 132 C; 105 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 435; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.4e-111;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGGTTTACAGCATGCCGCCACCCACC 60
Db 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGGTTTACAGCATGCCGCCACCCACC 60

QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 120
Db 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 120

QY 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180

QY 181 TCTGAAACGTTTGACGCCGAGGAGCTGCATCCCTGCGACACTCGCTGAAGCTGTACAAA 240
Db 181 TCTGAAACGTTTGACGCCGAGGAGCTGCATCCCTGCGACACTCGCTGAAGCTGTACAAA 240

QY 241 CAGGCTTTGCGGGGAGCCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGCTTTGCGGGGAGCCTCATCAAGCTCGAAGCCCTTGACCATGATGCCAGCCAC 300

QY 301 TACAAGCAGCACTGCCGCCCCACCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
Db 301 TACAAGCAGCACTGCCGCCCCACCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360

QY 361 AAAAGTTTCAAAAAGAACCTGGAAGATTCTTGTTTGAGATCCCGTTTGACTGTGGAG 420
Db 361 AAAAGTTTCAAAAAGAACCTGGAAGATTCTTGTTTGAGATCCCGTTTGACTGTGGAG 420

QY 421 CCAGCCCAAGAGTAA 435
Db 421 CCAGCCCAAGAGTAA 435

RESULT 2
ID AAF28953
XX AAF28953 standard; DNA; 435 BP.
XX
AC AAF28953;
XX
DT 18-JUN-2002 (first entry)
XX
DE Equine granulocyte-macrophage colony stimulating factor gene.
XX
KW Immunostimulatory; granulocyte-macrophage colony stimulating factor;
KW horse; reverse transcriptase PCR; colony formation; blood; cytotoxicity;

KW inflammation; vector; adjuvant; immunogen; vaccination; vaccine;
KW equine herpes; tetanus; Borrelia burgdorferi; rabies; gene; ds.
OS Equus sp.
XX
XX Key Location/Qualifiers
CDS 1..435
FT /*tag= a
FT /product= "equine GM-CSF"
XX
XX WO200077210-A1.
XX
XX 21-DEC-2000.
XX
XX 08-JUN-2000; 2000WO-FR001590.
XX
XX 10-JUN-1999; 99US-0138843P.
XX
XX (MERI-) MERIAL.
XX
XX Bublot M, Perez JM, Andreoni CMP;
XX
XX WPI; 2001-080689/09.
XX
XX P-PSDB; AAB37147.
XX
XX Novel DNA encoding equine granulocyte-macrophage colony-stimulating
XX factor, useful as adjuvant for vaccines and as non-specific
XX immunostimulant.
XX
XX Claim 3; Fig 1; 34pp; French.
XX
XX This sequence represents the gene encoding a horse granulocyte-macrophage
XX colony stimulating factor (GM-CSF). The gene was isolated from horse
XX lymphocytes using a reverse transcriptase PCR method with primers
XX AAF28954-AAF28960. GM-CSF induces colony formation in various types of
XX blood cells and particularly induces cytotoxicity of macrophages;
XX stimulates antibody-dependent cytotoxicity, and causes recruitment of
XX leucocytes to sites of inflammation. Vectors containing the gene or the
XX protein itself, are useful as adjuvants in immunogenic or vaccinating
XX compositions for horses, e.g. for protection against equine herpes,
XX tetanus, Borrelia burgdorferi, rabies etc. Also as non-specific
XX stimulators of the immune system. In a specific example, plasmid pJP097,
XX containing the sequence for equine GM-CSF was used to transform CHO-K1
XX cells and the transformants grown for 48 hours. The culture supernatant
XX was then added to culture medium being used to grow porcine bone marrow
XX cells. After 14 days, the mean number of colonies per culture box was 12-
XX 15, compared with none for cells grown in absence of GM-CSF. Equine GM-
XX CSF allows a reduction in the amount of immunogenic/vaccinating component
XX required, and may induce a response in animals that would otherwise be
XX non-responders
XX
SQ Sequence 435 BP; 109 A; 132 C; 105 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 435; DB 4; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.4e-111;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGGTTTACAGCATGCCGCCACCCACC 60
Db 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGGTTTACAGCATGCCGCCACCCACC 60

QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 120
Db 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 120

QY 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 AGCCTTCTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180

QY 181 TCTGAAACGTTTGACGCCGAGGAGCTGCATCCCTGCGACACTCGCTGAAGCTGTACAAA 240
Db 181 TCTGAAACGTTTGACGCCGAGGAGCTGCATCCCTGCGACACTCGCTGAAGCTGTACAAA 240

QY 241 CAGGGCTTGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAC 300
 Db |||||
 QY 241 CAGGGCTTGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAC 300
 Db |||||
 QY 301 TACAGCAGCACTGCCCCCACCCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
 Db |||||
 QY 301 TACAGCAGCACTGCCCCCACCCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
 Db |||||
 QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
 Db |||||
 QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
 Db |||||
 QY 421 CCAGCCCAAGTAA 435
 Db |||||
 QY 421 CCAGCCCAAGTAA 435
 Db |||||

RESULT 3
 AAQ24294
 ID AAQ24294 standard; DNA; 432 BP.
 AC AAQ24294;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-OCT-1992 (first entry)
 XX
 DE Ovine GM-CSF gene.
 XX
 KW Granulocyte-macrophage colony-stimulating factor; immuno-depression;
 KW vaccine adjuvants; cytokine; ss.
 OS
 XX Ovis aries.
 FH Key
 FT CDS
 FT 1..432
 FT /tag= c
 FT /note= "ovine GM-CSF"
 FT sig_peptide
 FT 1..51
 FT /tag= a
 FT /note= "putative signal sequence"
 FT misc_feature
 FT 1..25
 FT /tag= d
 FT /note= "GM-N PCR primer"
 FT mat_peptide
 FT 52..432
 FT /tag= b
 FT /note= "mature protein"
 FT misc_feature
 FT 408..432
 FT /tag= e
 FT /note= "GM-C PCR primer"

PN W09205255-A.
 XX
 PD 02-APR-1992.
 XX
 PF 13-SEP-1990; 90AU-00002294.
 XX
 PR 13-SEP-1990; 90AU-00002294.
 PR 21-MAR-1991; 91AU-00005175.
 XX
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX
 PI Wood PR, Rothe JS, Seow HF;
 XX
 DR WPI: 1992-150483/18.
 DR P-PSDB; AAR23662.
 XX
 PT DNA encoding ovine cytokine(s) - used to prepare recombinant cytokine(s)
 PT for treatment of immuno-depression in sheep.
 PS Claim 2; Fig 3; 79pp; English.
 XX
 CC The sequence is that of the ovine granulocyte-macrophage colony
 CC stimulating factor (GM-CSF) gene which can be used in the prodn. of

CC recombinant gamma-interferon, a cytokine-like molecule. The ovine
 CC cytokines will be useful in the intensive livestock industries such as
 CC live animal export trade, feed-lots and intensive rearing industries,
 CC where animals are subjected to great environmental challenge with
 CC infectious diseases, partic. respiratory infections, and are more prone
 CC to immunodepressive effects. The cytokines may be used for treatment or
 CC prophylaxis to maintain, stimulate or enhance immunoresponsiveness. They
 CC may also be useful as natural adjuvants for vaccines for sheep and
 CC cattle. See also AAQ24293-305, AAQ2311-15, AAQ24317-18 and AAQ25857-58.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX

SQ Sequence 432 BP; 101 A; 138 C; 103 G; 90 T; 0 U; 0 Other;

Query Match 83.5%; Score 363.2; DB 2; Length 432;
 Best Local Similarity 90.0%; Pred. No. 1.8e-91;
 Matches 389; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCATCTGGTTTACAGCATGCCGACCCACC 60
 Db |||||
 QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCATCTGGTTTACAGCATGCCGACCCACC 60
 Db |||||
 QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
 Db |||||
 QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
 Db |||||
 QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAAACAGTAGAAGTCGTC 180
 Db |||||
 QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAAACAGTAGAAGTCGTC 180
 Db |||||
 QY 181 TCTGAAAGCTTTGACGCGCAGGAGCTGACATGCCCTGCAGACTCGCCTGAAGCTGTACAA 240
 Db |||||
 QY 181 TCTGAAAGCTTTGACCTCCAGGAGCCGACATGCCCTGCAGACTCGCCTGTGAGCTGTACAAG 240
 Db |||||
 QY 241 CAGGGCTTGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAC 300
 Db |||||
 QY 241 CAGGGCTTGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCGCCAC 300
 Db |||||
 QY 301 TACAAAGCAGCACTGCCCCCACCCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
 Db |||||
 QY 301 TACAAAGCAGCACTGCCCCCACCCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
 Db |||||
 QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
 Db |||||
 QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
 Db |||||
 QY 421 CCAGCCCAAGTAA 432
 Db |||||
 QY 421 CCAGCCCAAGTAA 432
 Db |||||

RESULT 4
 ABZ80827
 ID ABZ80827 standard; DNA; 435 BP.
 XX
 AC ABZ80827;
 XX
 DT 11-SEP-2003 (revised)
 DT 27-JUN-2003 (first entry)
 XX
 DE Feline granulocyte-macrophage colony stimulating factor gene 3R4.
 XX
 KW Granulocyte-macrophage colony stimulating factor; GM-CSF; ds; gene;
 KW antibacterial; antiviral; vaccine; animal; immunogen; DMRIE;
 KW cationic lipid; quaternary ammonium salt; canine distemper virus;
 KW canine parainfluenza virus; canine herpes virus; feline herpes virus;
 KW equine herpes virus; dog; cat; horse.
 OS
 XX Felis catus.
 FH Key
 FT CDS
 FT 1..435
 FT /tag= a
 FT /product= "feline GM-CSF 3R4"

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XX WO200077043-A2.
XX PD 21-DEC-2000.
XX PF 08-JUN-2000; 2000WO-FR001592.
XX PR 10-JUN-1999; 99FR-00007604.
XX PR 19-JUL-1999; 99US-0144490P.
XX PA (MERI-) MERIAL.
XX PI Fischer LJ, Barzu-Le Roux S, Audonnet JF;
XX WPI; 2001-071259/08.
XX DR P-PSDB; AHP98710.
XX PT DNA vaccine containing plasmid and cationic lipid containing quaternary
XX PT ammonium salt; useful for protecting pets and sports animals against,
XX PT e.g. herpes virus.
XX PS Example 9; Fig 24; 109pp; French.
XX CC The invention relates to a novel DNA vaccine against pathogens that
XX CC affect pets and sports animals comprises a plasmid containing a sequence,
XX CC expressible in vivo, that encodes an immunogen from the relevant pathogen
XX CC and a cationic lipid containing a quaternary ammonium salt, particularly
XX CC N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium
XX CC (DMRIE). The immunogens are particularly taken from canine distemper
XX CC virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes
XX CC virus (CHV), feline herpes virus type 1 (FHV-1), equine herpes virus type
XX CC 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of
XX CC an immunogenic stimulation factor especially a granulocyte-macrophage
XX CC colony stimulation factor (GM-CSF) to enhance the immunogenic response.
XX CC The vaccines, which may be multivalent, are particularly used to protect
XX CC dogs, cats and horses against bacterial and viral diseases, particularly
XX CC those caused by the Paramyxoviridae. Formulations with the quaternary
XX CC ammonium salt provide a better immune response and thus more efficient
XX CC protection, particularly when administered subcutaneously. This sequence
XX CC represents the gene encoding a feline GM-CSF used in the invention.
XX CC (Updated on 11-SEP-2003 to standardise OS field)
XX SQ Sequence 435 BP; 116 A; 121 C; 102 G; 96 T; 0 U; 0 Other;

Query Match 76.5%; Score 332.6; DB 4; Length 435;
Best Local Similarity 85.3%; Pred. No. 7e-83;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCAGCTGTGTTTACAGCATGCCGCCACCCACC 60
DB 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCAGCTGTGTTTACAGCATCTCTGCACCCACC 60
QY 61 CGCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
DB 61 AGTTCAACCAGCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCTCTG 120
QY 121 AGCCTTCTGAACAACAGTAGTGAACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
DB 121 AGCCTTCTGAACAACAGTAGTGAACACTGCTGTATGAATGAACAGTAGAAGTCGTC 180
QY 181 TCTGAACGTTTTCGCCGAGGAGCTGCATCCCTGCGAGACTCGCTGAAGCTGTACAAA 240
DB 181 TCTGAACGTTTTCGCCGAGGAGCTGCATCCCTGCGAGACTCGCTGAAGCTGTACGAG 240
QY 241 CAGGGCTTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGCACCATGATGCCAGCCAC 300
DB 241 CAGGGCTTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGCAGGATGATGCCAACCAT 300
QY 301 TACAAGCAGCACTGCCGCCACCCCTTCTGTGTGAACCCAGCATGATCACTTC 360
DB 301 TACAAGCAGCACTGCCGCCACCCCTTCTGTGTGAACCCAGCATGATCACTTC 360
QY 361 AAAAGTTTCAAAAAAGAACCTGAAGGATTTTCTGTGTTTGTAGATCCCGCTTGTGACTGCTGGAAG 420
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DB 361 AAAAATTTCAAGAGAAATCTGAAGGATTTTCTGTTTACATCCCTTTGACTGCTGGAAG 420
QY 421 CCAGCCCAAGAGTAA 435
DB 421 CCAGTCAAGAAAGTGA 435

RESULT 5
ID AAZ55575 standard; cDNA; 444 BP.
XX AAZ55575;
XX AC AAZ55575;
XX DT 14-MAR-2000 (first entry)
XX DE Feline GMCSF cDNA.
XX KW Granulocyte macrophage colony-stimulating factor; GMCSF; antibody;
XX KW feline; inhibitor; immune response; immunoregulation; tumour; cancer;
XX KW autoimmune disease; vaccine; ss.
XX OS Felis catus.
XX FH Key Location/Qualifiers
XX FT CDS 10..444
XX FT /*tag= a
XX FT /product= "Feline GMCSF"
XX PN WO9961618-A2.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US011942.
XX PR 29-MAY-1998; 98US-0087306P.
XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX DR P-PSDB; AAY58229.
XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX PT useful for treating or preventing e.g. tumors or autoimmune disease.
XX PS Claim 1k; Page 251-252; 264pp; English.
XX CC Sequences AAZ55575-255580 represent cDNA sequences encoding feline
XX CC granulocyte macrophage colony-stimulating factor (GMCSF). The invention
XX CC relates to canine interleukin-4 (IL-4), canine or feline Flt-3 ligand,
XX CC canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5,
XX CC canine IL-13, feline interferon-alpha (IFN-alpha) and feline GMCSF, and
XX CC nucleotides which encode these immunoregulatory proteins. The proteins,
XX CC their associated nucleic acids, specific antibodies and inhibitors may be
XX CC used as vaccines for therapeutic or prophylactic regulation of an immune
XX CC response in animals (particularly cats, dogs, horses and humans). They
XX CC may be used to treat autoimmune or infectious diseases including
XX CC allergies, tumours, inflammation and graft rejection, and to increase the
XX CC response from a co-administered antigen. The nucleotide sequences can
XX CC also be used for the recombinant production of a protein, while
XX CC nucleoside fragments are useful as probes, as amplification primers and
XX CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX CC The proteins may be used to raise antibodies and to screen for modulators
XX CC of activity, while the antibodies may be used in detection, and in drug
XX CC targeting
XX SQ Sequence 444 BP; 119 A; 127 C; 104 G; 94 T; 0 U; 0 Other;

Query Match 76.5%; Score 332.6; DB 3; Length 444;
Best Local Similarity 85.3%; Pred. No. 7e-83;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
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QY 1 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 60
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DB 70 AGTTCAACCCAGCTCTGTCTACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGGCCCTG 129
QY 121 AGCCTTCTCAACAACTAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
DB 130 AGCCTTCTGAACAACTAGTAGTGAATACTGTGTGATGAATGAACAGTAGAAGTCGTC 189
QY 181 TCTGAAACGTTTACGCCGAGGAGCTGACATGCTTGCAGACTGCGCTGAAGCTGTACAAA 240
DB 190 TCTGAAATGTTGACCTCGAGGCGGAATGCTTGCAGACTCACCTAAGCTGTACGAG 249
QY 241 CAGGCTTCGGGGGAGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
DB 250 CAGGCTTCAGGGGAGGCTCATCAAGCTCAAGGAGCCCTTGAGATGATGCCAACCAT 309
QY 301 TACAAGCAGACTGCCCCCCCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTC 360
DB 310 TACAAGCAGACTGCCCCCTTACTCGGAACGCCCTGTGAAACCCAGACTATCACTTC 369
QY 361 AAAAGTTTCAAAAGAACCTGGAAGGATTTCTGTTTGTAGATCCCGTTTGACTGCTGGAAG 420
DB 370 AAAAATTTCAAAAGAGAACTGGAAGGATTTCTGTTTAAACAACCCCTTGTACTGCTGGGA 429
QY 421 CCAGCCCAAGTA 435
DB 430 CCAGACCAGAGTAA 444

RESULT 6
AAZ55576/c
ID AAZ55576 standard; cDNA; 444 BP.
XX
AC AAZ55576;
XX
DT 14-MAR-2000 (first entry)
XX
DE Feline GMCSF cDNA complement.
XX
KW Granulocyte macrophage colony-stimulating factor; GMCSF; antibody;
KW feline; inhibitor; immune response; immunoregulation; tumour; cancer;
KW autoimmune disease; vaccine; ss.
XX
OS Felis catus.
FH Key Location/Qualifiers
FT CDS complement(1..435)
FT /*tag= a
FT /*product= "Feline GMCSF"
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US011942.
XX
PR 29-MAY-1998; 98US-0087306P.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR P-PSDB; AAY58229.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease.
XX

PS Claim 1k; Page 253; 264pp; English.
XX Sequences AAZ55575-255580 represent cDNA sequences encoding feline
CC granulocyte macrophage colony-stimulating factor (GMCSF). The invention
CC relates to canine interleukin-4 (IL-4), canine or feline flt-3 ligand,
CC canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5,
CC canine IL-13, feline interferon-alpha (IFN-alpha) and feline GMCSF, and
CC nucleotides which encode these immunoregulatory proteins. The proteins,
CC their associated nucleic acids, specific antibodies and inhibitors may be
CC used as vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans). They
CC may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase the
CC response from a co-administered antigen. The nucleotide sequences can
CC also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for modulators
CC of activity, while the antibodies may be used in detection, and in drug
CC targeting
XX
SQ Sequence 444 BP; 94 A; 104 C; 127 G; 119 T; 0 U; 0 Other;
Query Match 76.5%; Score 332.6; DB 3; Length 444;
Best Local Similarity 85.3%; Pred. No. 7e-83;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 1 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 60
DB 435 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATCTCTGCACCCACC 376
QY 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB 375 AGTTCAACCCAGCTCTGTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGGCCCTG 316
QY 121 AGCCTTCTGAACAACTAGTAGTACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
DB 315 AGCCTTCTGAACAACTAGTAGTGAATACTGTGTGATGAATGAACAGTAGAAGTCGTC 256
QY 181 TCTGAAACGTTTACGCCGAGGAGCTGACATGCCCTGCAGACTCGCTGAAGCTGTACAAA 240
DB 255 TCTGAAATGTTTGACCTCGAGGAGCGGAATGCCCTGCAGACTCACCTAAGCTGTACGAG 196
QY 241 CAGGCTTCGGGGGAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300
DB 195 CAGGCTTCAGGGGAGGCTCATCAAGCTCAAGGAGCCCTCTGAGAATGATGCCAACCAT 136
QY 301 TACAAGCAGACTGCCCCCCCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTC 360
DB 135 TACAAGCAGACTGCCCCCTTACTCGGAACGCCCTGTGAAACCCAGACTATCACTTC 76
QY 361 AAAAGTTTCAAAAGAACCTGGAAGGATTTCTGTTTGTAGATCCCGTTTGACTGCTGGAAG 420
DB 75 AAAAATTTCAAAAGAGAACTGGAAGGATTTCTGTTTAAACAACCCCTTGTACTGCTGGGA 16
QY 421 CCAGCCCAAGTA 435
DB 15 CCAGACCAGAGTAA 1
RESULT 7
AAQ64864
ID AAQ64864 standard; DNA; 798 BP.
XX
AC AAQ64864;
XX
DT 25-MAR-2003 (revised)
DT 10-MAR-2003 (revised)
DT 07-NOV-1994 (first entry)
XX
DE CHEF-2 gene.
XX
KW Cytokine; chimerism enhancing factors; porcine; transplant;

KW xenogeneic cells; bone marrow; African swine fever; Hog cholera;
XX Pseudorabies; ss.
OS

XX Sus scrofa.

XX Key Location/Qualifiers
FT sig_peptide 30..99
FT /tag= a
FT /note= "signal"
FT mat_peptide 100..464
FT /tag= b

XX WO9409803.A1.

XX 11-MAY-1994.

XX 26-OCT-1993; 93WO-US010295.

XX 27-OCT-1992; 92US-00967188.

XX 08-OCT-1993; 93US-00133979.

XX (BIOT-) BIOTRANSPLANT INC.

XX Ponath PD, Rosa MD, Monroy RL, Schacter BZ, Hawley RJ;

XX WPI; 1994-167114/20.

XX P-PSDB; AAR54818.

XX Porcine cytokine Chimerism Enhancing Factors (CHEFs) and DNA - used to
XX enhance xenograft tolerance.

XX Claim 40; Page 72; 113pp; English.

XX The sequence is that of a porcine cytokine gene designated chimerism
XX enhancing factor (CHEF-2). The cytokine can be used for improving
XX engraftment, stabilisation and proliferation of tissues, esp. bone marrow
XX cells, in xenogeneic transplantation. The cytokine may be used to prevent
XX or treat various swine diseases, e.g. African swine fever, Hog cholera,
XX Pseudorabies, etc. See also AAQ64863-80. (Updated on 10-MAR-2003 to add
XX missing OS field.) (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 798 BP; 208 A; 215 C; 180 G; 195 T; 0 U; 0 Other;

Query Match 76.5%; Score 332.6; DB 2; Length 798;
Best Local Similarity 85.3%; Pred. No. 8.8e-83;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGGTTTACAGCATGCCGCCACCCACC 60

DB 30 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGGTTTACAGCATGCCGCCACCCACC 89

QY 61 CQCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTTG 120

DB 90 CGCCACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTTG 149

QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGTAGTCGTC 180

DB 150 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGTAGTCGTC 209

QY 181 TCTGAACGTTTGAACCGCAGGAGCTGCATCGCTGCAGACTCGCTGAAGCTGTACAAA 240

DB 210 TGTGAAATGTTTGAACCGCAGGAGGACATCGGTGCAGACTCGCTGAACTGTACAA 269

QY 241 CAGGCTTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300

DB 270 CAGGCTTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 329

QY 301 TACAAGCAGACTGCCCCCCCACCTCTGTGAAACCTTCTGTGAAACCCAGATGATCCTTC 360

DB 330 TATGAGCAGACTGCCCCCCCACCTCTGTGAAACCTTCTGTGAAACCCAGATGATCCTTC 389

QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCCTGTGTTGAGATCCCGTTTCACTGCTGGAAG 420

DB 390 AAAAGTTTCAAAAGACAGTCTGAACAATAATTTCTTTTACCATCCCTTTGACTGCTGGGG 449

QY 421 CCAGCCAGCAAGTAA 435

DB 450 CCAGTCAAAAAGTAA 464

RESULT 8

ADQ76022

ID ADQ76022 standard; DNA; 435 BP.

XX ADQ76022;

XX 07-OCT-2004 (first entry)

XX Human GM-CSF wild-type coding sequence.

XX ds; gene; human; GM-CSF; codon optimisation; protein production.

XX Homo sapiens.

XX WO2004059556-A2.

XX 15-JUL-2004.

XX 23-DEC-2003; 2003WO-EP014850.

XX 23-DEC-2002; 2002DE-01060805.

XX (GENE-) GENEART GMBH.

PI Raab D, Graf M, Notka F, Wagner R;

XX WPI; 2004-543639/52.

XX Computer optimization of a nucleotide sequence for a protein comprises

PT evaluating test sequences with a quality function to determine the

PT optimum sequence.

XX Disclosure; SEQ ID NO 1; 83pp; German.

XX The present invention relates to a method of optimising a coding sequence
CC for expression of a protein, based on the amino acid sequence of the
CC protein. This involves the use of a computer to generate a test sequence
CC with m optimisation positions determined for a defined region, in which
CC positions the codon usage is varied. The optimum codon usage at such
CC positions is determined by means of a power function. The steps are
CC reiterated with different regions of the sequence, with the optimised
CC codons previously identified being left unchanged during subsequent
CC steps. The method can be used for expression of proteins. The present
CC sequence is the human GM-CSF wild-type coding sequence.

XX Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;

Query Match 76.2%; Score 331.6; DB 12; Length 435;
Best Local Similarity 85.3%; Pred. No. 1.3e-82;
Matches 370; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGGTTTACAGCATGCCGCCACCCACC 60

DB 1 ATGTGGCTGCAGAGCTGCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 60

QY 61 CGCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTTG 120

DB 61 CGCTCGCCAGCCCGCAGCAGCCCTGGGAGCATGGAATGCCATCCAGGAGGCCCG 120

QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTATCATGAATGAACAGTAGTAGTCGTC 180

DB 121 CGTCTCTTGAACCTCAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGTAGTC 180

QY 181 TCTGAAAACGTTTGAACCGCAGGAGGAGTGATGCCCTGCGAGACTCGGCTGAAGCTGTACAA 240

DB 181 TCAGAAATGTTTGAACCTCCAGGAGCCGACCTGCCTACAGACCCCGCTGGAGCTGTACAAG 240

QY 241 CAGGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
 DB AEF81846 standard; DNA; 435 BP.
 AC AEF81846;
 DT 20-APR-2006 (first entry)
 DE Human GM-CSF wild-type (10CpG) DNA.
 DE ds; gene; vector; expression; GM-CSF.
 KW Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 1..435
 FT /*tag= a
 FT /product= "GM-CSF"
 PN WO2006015789-A2.
 XX 16-FEB-2006.
 XX 03-AUG-2005; 2005WO-EP008423.
 XX 03-AUG-2004; 2004DE-10037611.
 XX 03-AUG-2004; 2004DE-10037652.
 XX (GENE-) GENEART GMBH.
 PA Notka F, Graf M, Leikam D, Wagner R, Raab D;
 PI WPI; 2006-193389/20.
 DR P-PSDB; AEF81847.
 DR GENBANK; M11220.
 XX
 PT Process to modify nucleic acid for incorporation in a vectored expression
 PT in e.g. transgenic animals, medical therapy or vaccines.
 XX
 PS Example 3; SEQ ID NO 23; 99pp; German.
 XX
 CC This invention describes a novel process for modifying nucleic acid for a
 CC vectored expression modulation by targeted insertion or removal of CpG di-
 CC nucleotides. The invention also describes modified nucleic acids and
 CC vector expressions. The process commences with the expression from tissue
 CC of a sample substance containing the target nucleic acid sequence,
 CC followed by its modification to increase or decrease the genetic
 CC expression of CpG di-nucleotides present, by degeneration of the genetic
 CC code. The modified target nucleic acid sequence is cloned with the
 CC modified number of CpG di-nucleotides in a suitable vector expression,
 CC operationally linked with a suitable transcription regulatory sequence.
 CC The modified target nucleic acid sequence is then expressed in a modified
 CC expression system. The novel process can be used to modify nucleic acids
 CC for incorporation in a vectored expression in e.g. transgenic animals,
 CC medical therapy or vaccines. The process extends the usable range of

CC Genetic expression. This sequence encodes human wild-type GM-CSF
 CC containing 10CpG, used in the process of the invention.
 XX
 SQ Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;
 Query Match 76.2%; Score 331.6; DB 15; Length 435;
 Best Local Similarity 85.3%; Pred. No. 1.3e-82;
 Matches 370; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 1 ATGTGGCTGCAGAACCTCTCTCTCTGGGACTGTGGTTTACAGATGCCAGCCACCC 60
 DB 1 ATGTGGCTGCAGAGCTCTCTCTCTGGGACTGTGGTTTACAGATGCCAGCCACCC 60
 QY 61 CGCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
 DB 61 CGCTCGCCAGCCCGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG 120
 QY 121 AGCTTCTGAACACAGTAGTAGACTGCTGCTGCTATCATGAATGAACACAGTAGAAGTCGTC 180
 DB 121 CGTCTCTGAAACCTTGAGTAGAGACACTGCTGCTGAGATGAATGAACACAGTAGAAGTCATC 180
 QY 181 TCTGAACGTTTTCACGCGGAGGAGCTGACATGCCCTGCAGACTCGCCTGGAAGCTGTACAAA 240
 DB 181 TCAGAAATGTTTTCACCTCCAGAGCCGACCTGCTTACAGACCCGCTGGAGCTGTACAA 240
 QY 241 CAGGCTTTCGCGGGCAGGCTCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
 DB 241 CAGGCTTTCGCGGGCAGGCTCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
 QY 301 TACAAGACGACCTGCCCCCCCCCAGCCCTGGAATCTCTGTGCAACCCAGATGACCTTC 360
 DB 301 TACAAGACGACCTGCCCCCCCCCAGCCCTGGAATCTCTGTGCAACCCAGATGACCTTC 360
 QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTCTGTTTGAATCCCGTTTGACTGCTGGAG 420
 DB 361 GAAAGTTTCAAAAAGAACCTGAAGGATTTCTGTTTGAATCCCGTTTGACTGCTGGAG 420
 QY 421 CCAGCCCAAGAGTA 434
 DB 421 CCAGTCCAGGAGTA 434
 RESULT 10
 AAF55040
 ID AAF55040 standard; DNA; 432 BP.
 XX
 AC AAF55040;
 XX
 DT 15-MAY-2001 (first entry)
 XX
 DE Nucleotide sequence of GM-CSF gene clone 3R4.
 XX
 KW Capsid protein; FCV strain 431; FCV strain G1; vaccine; cat; ds.
 XX
 OS Felis catus.
 FH Key Location/Qualifiers
 FT CDS 1..432
 FT /*tag= a
 FT /product= "GM-CSF"
 FT
 FT WO200105934-A2.
 XX
 PD 25-JAN-2001.
 XX
 PF 13-JUL-2000; 2000WO-FR002051.
 XX
 PR 16-JUL-1999; 99FR-00009421.
 PR 11-FEB-2000; 2000FR-00001761.
 XX
 PA (MERI-) MERIAL.
 XX
 PI Audonnet JF, Baudu PGN, Brunet SC;

CC N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanammonium
CC (DMRIE). The immunogens are particularly taken from canine distemper
CC virus (CDV), canine parainfluenza virus type 2 (CPI-2), canine herpes
CC virus (CHV), feline herpes virus type 1 (FHV-1), equine herpes virus type
CC 1 (EHV-1), and EHV type 4 (EHV-4). The method may also include the use of
CC an immunogenic stimulation factor especially a granulocyte-macrophage
CC colony stimulation factor (GM-CSF) to enhance the immunogenic response.
CC The vaccines, which may be multivalent, are particularly used to protect
CC dogs, cats and horses against bacterial and viral diseases, particularly
CC those caused by the Parvoviridae. Formulations with the quaternary
CC ammonium salt provide a better immune response and thus more efficient
CC protection, particularly when administered subcutaneously. This sequence
CC represents the gene encoding a feline GM-CSF used in the invention.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 435 BP; 117 A; 120 C; 101 G; 97 T; 0 U; 0 Other;

Query Match 76.1%; Score 331; DB 4; Length 435;
Best Local Similarity 85.1%; Pred. No. 2e-82;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCGCCACCCACC 60
DB 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCGCCACCCACC 60
QY 61 CGCCAAACCAGCCCTGCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB 61 AGTTCAACCAGCTGTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
DB 121 AGCCTTCTGAACAACAGTAGTGAAATACTGTGTGATGAATGAAGCAGTAGAAGTCGTC 180
QY 181 TCTGAAACGTTTGACCGCGAGGAGCTGACATCCCTGCAGACTCGCCTGAAGCTGTACAAA 240
DB 181 TCTGAAATGTTTGACCTTGAGGAGCGGAAATGCCTGCAGACTCACCTAAAGCTGTACGAG 240
QY 241 CAGGCTTCGCGGGCAGCTCATCAAGTCGAGGCCCTTCACCATGATGCCAGCCAC 300
DB 241 CAGGCTTCACGGGCGAGCTCATCAAGCTTCACAGGAGCCTCTGAGAATGATGCCAACCAT 300
QY 301 TACAAGCAGCACTGCCGCCACCCCTCGAAACTTCTGTGCAACCCAGATGATCACTTC 360
DB 301 TACAAGCAGCACTGCCCTTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 360
QY 361 AAAATTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTGACTGCTGGAG 420
DB 361 AAAAATTTCAAGAGAACTGAAGATTTCTGTTTAAACATCCCTTTGACTGCTGGAAA 420
QY 421 CCAGCCCAAGTAA 435
DB 421 CCAGTCAAGAGTGA 435

RESULT 14
ACCT78877
ID ACC78877 standard; DNA; 435 BP.
XX
AC ACC78877;
XX
DT 02-SEP-2003 (first entry)
XX
DE Human GM-CSF encoding DNA.
XX
KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
KW granulocyte-macrophage colony stimulating factor; GM-CSF; human; gene;
KW ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..435
FT /*tag= a

FT
XX
PN W02003031464-A2.
XX
PD 17-APR-2003.
XX
PF 09-OCT-2002; 2002WO-US032263.
XX
PR 10-OCT-2001; 2001US-0328523P.
PR 19-OCT-2001; 2001US-0344692P.
PR 28-NOV-2001; 2001US-0334233P.
PR 07-JUN-2001; 2001US-0334301P.
PR 07-JUN-2002; 2002US-0387292P.
PR 25-JUN-2002; 2002US-0391777P.
PR 17-JUL-2002; 2002US-0396594P.
PR 16-AUG-2002; 2002US-0404249P.
PR 28-AUG-2002; 2002US-0407527P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI De Fries S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX
DR WPI; 2003-449162/42.
DR P-PSDB; ABR55847.
XX
PT Remodeling a peptide, by removing a saccharyl subunit from the peptide to
PT form truncated glycan, and adding or deleting glycosyl groups to a
PT peptide and/or adding modifying group of a peptide to remodel the
PT peptide.
XX
PS Example; Fig 59A; 900pp; English.
XX
CC The invention relates to a cell-free, in vitro method of remodeling a
CC peptide. The method involves removing a saccharyl subunit from the
CC peptide, thus forming a truncated glycan, and contacting the truncated
CC glycan with at least one glycosyltransferase and at least one glycosyl
CC donor under conditions suitable to transfer at least one glycosyl donor
CC to the truncated glycan, thus remodeling the peptide. Conjugates can be
CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,
CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
CC peptide, interferon-gamma peptide, alpha-1-proteinase inhibitor (A-1-PI)
CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
CC glycoprotein IIb/IIIa monoclonal antibody peptide, chimeric anti HER2
CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
CC CD20 antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide,
CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth
CC hormone (HGH) peptide, and a modifying group, where the modifying group
CC is covalently attached to the peptide through an intact glycosyl linking
CC group. The method is useful for a cell-free, in vitro method of
CC remodeling the above mentioned peptides. The present sequence represents
CC a human GM-CSF encoding DNA
XX
SQ Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;

Query Match 76.1%; Score 331; DB 10; Length 435;
Best Local Similarity 85.1%; Pred. No. 2e-82;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGATGCCGCCACCCACC 60
DB 1 ATGTGGCTGCAGAGCCTGCTGCTTGTGGGCACCTGTGGCCTGCAGCATCTCTGCACCCGCC 60
QY 61 CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB 61 CGCTCGCCCGCCCGCCAGCCAGCCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGCCCG 120
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
DB 121 CGTCTCTCTGAACCTTGAGTAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATC 180

QY 181 TCTGAACGTTTTCAGCGCCGAGGAGCTGACATGCTGCAGACTCGCTGAAGCTGTACAAA 240
DB 181 TCAGAAATGTTTGAACCTCCAGGAGCGGACCTGCCTACAGACCCGCTGGAGCTGTACAA 240
QY 241 CAGGGCTTCGGGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCGCCAGCCAC 300
DB 241 CAGGGCTTCGGGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCGCCAGCCAC 300
QY 301 TACAAGCAGCACTGGCCCCCCCCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTC 360
DB 301 TACAAGCAGCACTGGCCCCCCCCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTC 360
QY 361 AAAAGTTTCAAAAAGAACCTGGAAGATTTTCTGTTGAGATCCCGTTTCACTGCTGGAAG 420
DB 361 GAAAGTTTCAAAAAGAACCTGGAAGATTTTCTGTTGAGATCCCGTTTCACTGCTGGAAG 420
QY 421 CCAGCCCGAAGTAA 435
DB 421 CCAGTCCAGGAGTGA 435

RESULT 15

ADN49689
ID ADN49689 standard; DNA; 435 BP.

AC ADN49689;

DT 15-JUL-2004 (first entry)

DE Human granulocyte-macrophage colony stimulating factor DNA SeqID 17.

XX human; Gene; ds; erythropoietin; EPO; glycoconjugation;
KW glycopolyglycated EPO peptide; anaemia; antianaemic; haematocrit level;
KW kidney dialysis; haematology;

XX granulocyte-macrophage colony stimulating factor.

OS Homo sapiens.

XX WO2004033651-A2.

XX 22-APR-2004.

XX 08-OCT-2003; 2003WO-US031974.

XX 09-OCT-2002; 2002WO-US032263.

XX 05-NOV-2002; 2002US-00287994.

XX 06-JAN-2003; 2003US-00360770.

XX 19-FEB-2003; 2003US-00360779.

XX 09-APR-2003; 2003US-00410945.

XX (NEOS-) NEOSE TECHNOLOGIES INC.

XX De Fries S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;

XX WPI; 2004-399848/37.

XX P-PSDB; ADN49690.

XX Novel erythropoietin peptide comprising one or more glycans, having
PT glycoconjugate molecule covalently attached to peptide, useful for
PT treating anemia in mammal such as human.

XX Disclosure; SEQ ID NO 17; 1018pp; English.

XX This invention relates to novel erythropoietin (EPO) peptides and the
CC remodelling and glycoconjugation of these naturally occurring peptides
CC thereof. Specifically, each EPO peptide comprises one or more glycans and
CC has a glycoconjugate molecule such as polyethylene glycol (PEG) attached
CC to it. Accordingly, the present invention provides glycopeptidylated EPO
CC peptides that have either monoantennary, biantennary or triantennary
CC glycans covalently attached thereto. As such, these peptides are useful
CC for the treatment of anaemia, and hence exhibit antianaemic activities
CC working to increase haematocrit levels in mammals, in particular in

CC humans i.e. increasing the relative volume of blood occupied by
CC erythrocytes. Furthermore, EPO therapy can be used to treat kidney
CC dialysis patients. This polynucleotide is a human DNA sequence related to
CC the field of haematology, given in an exemplification of the invention.

XX Sequence 435 BP; 99 A; 140 C; 113 G; 83 T; 0 U; 0 Other;

Query Match 76.1%; Score 331; DB 12; Length 435;
Best Local Similarity 85.1%; Pred. No. 2e-82;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTGGGCACATGTGGTTTACAGATGCGCCGACCCACC 60

DB 1 ATGTGGCTGCAGAGCCTGTGCTCTTGGGCACATGTGGCCTGCAGCATCTCTGCACCCGCC 60

QY 61 GSCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120

DB 61 CGCTCGCCAGCCCCAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG 120

QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGT 180

DB 121 CGTCTCTGAACCTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180

QY 181 TCTGAACGTTTTCAGCGCCGAGGAGCTGACATGCTGTCAGACTCGCTGAAGCTGTACAAA 240

DB 181 TCAGAAATGTTTTCAGCCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAGCTGTACAA 240

QY 241 CAGGGCTTCGGGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCGCCAGCCAC 300

DB 241 CAGGGCTTCGGGGGAGAGCTCATCAAGCTCGAAGCCCTTGACCATGATGCGCCAGCCAC 300

QY 301 TACAAGCAGCACTGCCCCCCCCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTC 360

DB 301 TACAAGCAGCACTGCCCCCCCCCCTGGAACCTTCTGTGCAACCCAGATGATCACTTC 360

QY 361 AAAAGTTTCAAAAAGAACCTGGAAGATTTTCTGTTGAGATCCCGTTTCACTGCTGGAAG 420

DB 361 GAAAGTTTCAAAAAGAACCTGGAAGATTTTCTGTTGAGATCCCGTTTCACTGCTGGAAG 420

QY 421 CCAGCCCGAAGTAA 435

DB 421 CCAGTCCAGGAGTGA 435

Search completed: May 26, 2006, 00:41:08

Job time : 451 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 435

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Searched: 242596 seqs, 56442199 residues

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA_New.*

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09_NEW_PUB.seq.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US06_NEW_PUB.seq.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_NEW_PUB.seq.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	76.1	435	7	US-11-183-218-17
2	331	76.1	781	6	US-10-511-937-396
3	38.8	8.9	50	6	US-10-511-937-64
C 4	36.4	8.4	1109	6	US-10-468-193-113
C 5	33.8	7.8	2139	7	US-11-293-697-965
C 6	33.8	7.8	2243	7	US-11-293-697-1196
C 7	33.8	7.8	2562	7	US-11-293-697-1692
C 8	33.6	7.7	2062	7	US-11-293-697-1541
9	33.4	7.7	1628	6	US-10-953-349-35010
10	32.6	7.5	4611	7	US-11-267-871-717
11	32.6	7.5	4644	1	US-09-484-331-19
12	32.6	7.5	5247	1	US-09-484-331-20
C 13	32.6	7.5	5264	6	US-10-485-397-10
14	32.6	7.5	5314	1	US-09-484-331-27
C 15	32.6	7.5	5408	6	US-10-485-397-9
C 16	32.6	7.5	5715	7	US-11-258-392-4
C 17	32.6	7.5	7873	6	US-10-485-397-7
C 18	32.6	7.5	7943	6	US-10-485-397-8
19	32.6	7.5	9737	1	US-09-484-331-22
20	32.6	7.5	9737	1	US-09-484-331-23
21	32.6	7.5	9737	1	US-09-484-331-28
22	32.6	7.5	9871	1	US-09-484-331-24
23	32.6	7.5	10060	1	US-09-484-331-25
C 24	32.2	7.4	1973	6	US-10-505-928-462
25	32	7.4	3972	7	US-11-293-697-1765

26	31.8	7.3	1548	6	US-10-953-349-27676
C 27	31.6	7.3	5133	6	US-10-511-937-2799
28	31	7.1	632	6	US-10-953-349-28960
29	31	7.1	634	6	US-10-953-349-25300
C 30	31	7.1	3316	6	US-10-981-760-2
C 31	31	7.1	3331	6	US-10-953-349-8124
C 32	31	7.1	4644	1	US-09-484-331-19
C 33	31	7.1	5247	1	US-09-484-331-20
C 34	31	7.1	5314	1	US-09-484-331-27
C 35	31	7.1	6084	1	US-09-484-331-7
C 36	31	7.1	6085	1	US-09-484-331-8
C 37	31	7.1	6086	1	US-09-484-331-9
38	31	7.1	6629	6	US-10-946-650-49
C 39	31	7.1	6836	1	US-09-484-331-18
C 40	31	7.1	8540	7	US-11-183-218-57
41	31	7.1	8687	7	US-11-297-317-15
42	31	7.1	8687	7	US-11-297-317-16
C 43	31	7.1	9209	7	US-11-183-218-58
44	31	7.1	9362	7	US-11-297-317-18
45	31	7.1	9400	7	US-11-297-317-17

ALIGNMENTS

RESULT 1

US-11-183-218-17
; Sequence 17, Application US/11183218
; Publication No. US20060088906A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND
; FILE REFERENCE: 040853-01-5083-US02
; CURRENT APPLICATION NUMBER: US/11/183,218
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 10/410,945
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: PCT/US02/32263
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/334,301
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/334,233
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-183-218-17

Query Match 76.1%; Score 331; DB 7; Length 435;
Best Local Similarity 85.1%; Pred. No. 2.8e-85;

Matches	370;	Conservative	0;	Mismatches	65;	Indels	0;	Gaps	0;
Qy	1	ATGTGGCTGCAGAACCTGCTTTCTTTCTGGGCAC	CTGTGGTTTACAGCATGCCGACCCACCC	60					
Db	1	ATGTGGCTGCAGAGACCTGCTCTTTGGGCAC	CTGTGGCCTGCAGCATCTCTGCACCCGCC	60					
Qy	61	GGCCAA	CCGAGCCCTGTCACTCGGCGCCTGGCAGCATGTGGATGCCATCAAGAGGCGCC	120					
Db	61	CGCTCGCCAGCCCGACACGACGACGACCCCTGGAGCATGTGAATGCCATCCAGAGGCGCCG	120						
Qy	121	AGCCTCTTGAAACAA	CAGTAGTGACACTGCTGCTATCATGAATGAAACAGTAGTAGAGTCTCTC	180					
Db	121	CGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGTAGAGTCA	180						
Qy	181	TCTGAACAGTTTGAGGCGGAGGAGCTGCATGCCCTGCAGACTCGCCTGAAGCTGTACAAA	240						
Db	181	TCGAAATATGTTTGACCTCCAGGAGCGGACCTTGCCCTACAGACCCGCTGGAGCTGTACAA	240						
Qy	241	CAGGGCTTGCGGGG	CAGGCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCACAGCCAC	300					
Db	241	CAGGGCTTGCGGGG	CAGGCTCACCAAGCTCAAGGGCCCTTTGACCATGATGCCACAGCCAC	300					
Qy	301	TACAAGCAGCACTGCCCCCCCC	CACTTCTGTGTGAAACCCAGATGATCACTTC	360					
Db	301	TACAAGCAGCACTGCCCCCTCCAACCCCGGAAACTTCTGTGTGAAACCCAGATATCACTTC	360						
Qy	361	AAAAAGTTTCAAAA	GAAGACCTCAAGGATTTCTGTTTGATGATCCCGTTTGACTGCTGGGAG	420					
Db	361	GAAAGTTTCAAA	GAAGACCTCAAGGACTTTCTGCTTGTCATCCCTTTGACTGCTGGGAG	420					
Qy	421	CCAGCCCCAGAGTAA	435						
Db	421	CCAGTCCAGGAGTGA	435						

```

RESULT 2
US-10-511-937-396
; Sequence 396, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: Patent version 3.2
; SEQ ID NO 396
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-511-937-396

Query March 76.1%; Score 331; DB 6; Length 781;
Best Local Similarity 85.1%; Pred. No. 3.5e-85;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0

1 ATGTGGCTGCAGAACTCTTCTTCTGGGCACGTGGTTTACAGCATGCCGCCACC 60

```

Db	33	ATGTGGCTGCAGAGCCTGCTGCTCTTTGGGCACTGTGGGCTCGCAGCATCTCTGCACCCGGC	92
Qy	61	CGCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG	120
Db	93	CGCTCGCCAGCCCGCAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGCCCGG	152
Qy	121	AGCCTTCTGAACACAGTAGTGACACTGCTGCTCTATCATGAATGAACAAGTAGAAGTCGTC	180
Db	153	CGTCTCTCTGAACCTGTAGTAGAGACACTGCTGCTGAGATGAATGAACAAGTAGAAGTCATC	212
Qy	181	TCTGAACAGTTTGACGGCGAGGAGCTGACATGCTCTGCGAGACTCGCCTCAAGCTGTACAAA	240
Db	213	TCAGAAATGTTGACCTCCAGGAGCGACCTGCTCTACAGACCCGCTGGAGCTGTACAAG	272
Qy	241	CAGGCTTGGGGGAGCGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCACGCCAC	300
Db	273	CAGGCTTGGGGGAGCGCTCAACAAAGCTCAAGGGCCCTTGACCATGATGCCACGCCAC	332
Qy	301	TACAAGCAGCACTGCCCGCCCGCCACCTCGAAACTTCTGTGGAACCCAGATGATCACTTC	360
Db	333	TACAAGCAGCACTGCCCTCCAAACCCCGGAACTTCTGTGGAACCCAGATGATCACTTC	392
Qy	361	AAAAAGTTTCAAAAAGAACCTGAAGGATTTCTGTGTTGAGATCCCGTTTGCATGCTGGAG	420
Db	393	GAAAGTTTCAAGAGAGAACCTGAAGGACTTTCTGCTTGTGTCATCCCTTTGACTGCTGGAG	452
Qy	421	CCAGCCCAAGATAA 435	
Db	453	CCAGTCCAGGAGTGA 467	
RESULT 3			
US-10-511-937-64			
; Sequence 64, Application US/10511937			
; Publication No. US2006008836A1			
; GENERAL INFORMATION:			
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.			
; APPLICANT: Wohlgenuth, Jay			
; APPLICANT: Fry, Kirk			
; APPLICANT: Woodward, Robert			
; APPLICANT: Ly, Ngoc			
; APPLICANT: Prentice, James			
; APPLICANT: Morris, MacDonald			
; APPLICANT: Rosenberg, Steven			
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING			
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION			
; FILE REFERENCE: 506612000104			
; CURRENT APPLICATION NUMBER: US/10/511.937			
; CURRENT FILING DATE: 2004-10-19			
; PRIOR APPLICATION NUMBER: PCT/US2003/012946			
; PRIOR FILING DATE: 2003-04-24			
; PRIOR APPLICATION NUMBER: US 10/131,831			
; PRIOR FILING DATE: 2002-04-24			
; PRIOR APPLICATION NUMBER: US 10/325,899			
; PRIOR FILING DATE: 2002-12-20			
; NUMBER OF SEQ ID NOS: 3117			
; SOFTWARE: Patent in version 3.2			
; SEQ ID NO 64			
; LENGTH: 50			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-10-511-937-64			

```

Query Match      8.9%; Score 38.8; DB 6; Length 50;
Best Local Similarity 86.0%; Pred. No. 0.009;
Matches 43; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 316 CCCCCCACCCTGGAAACTTCTGTGCAACCCAGATGATCACCTTCAAAAG 365
      |||||
Db 1 CCTCCAACCCCGGAAACTTCTGTGCAACCCAGACTATCACCTTTGAAAG 50
      |||||

RESULT 4

```

US-10-468-193-1113/c
; Sequence 113, Application US/10468193
; Publication No. US20060100416A1
; GENERAL INFORMATION:
; APPLICANT: Palli, Subba R.
; APPLICANT: Cress, Dean E.
; APPLICANT: Fujimoto, Ted T.
; APPLICANT: Kumar, Mohan B.
; TITLE OF INVENTION: Novel Substitution Mutant Receptors and Their Use in A Nuclear
; TITLE OF INVENTION: Receptor-Based Inducible Gene Expression System
; FILE REFERENCE: A01247-US
; CURRENT APPLICATION NUMBER: US/10/468,193
; CURRENT FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/313,925
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US02/05090
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 113
; LENGTH: 1109
; TYPE: DNA
; ORGANISM: Nephrotetrix cincticeps
US-10-468-193-1113

Query Match 8.4%; Score 36.4; DB 6; Length 1109;
Best Local Similarity 49.0%; Pred. No. 0.15;
Matches 97; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
QY 104 CCATCAAGAGGCGCTTGTGAACAGTAGTGACACTGCTGTATCATGAATG 163
Db |||||
QY 829 CCTTCATGAGCAGATGATCGCGGAAACCGCAGCAGATCTTCGATGACTTCCCCACGC 770
Db |||||
QY 164 AAACAGTAGAGTCTCTCTGAAAGCTTTGACCGGAGGAGCTGACATGCTGCAGACTC 223
Db |||||
QY 769 CTGCCATCTGTACGACTCTCCGGTACGGCTGTTGTCGGAACAGGATCGAGTCTG 710
Db |||||
QY 224 GCCTGAAGCTGTACAAACAGAGGCTTTCGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGA 283
Db |||||
QY 709 TCTGGACGTGTACCTCCGCGCATCCGAGCATCATCACTCGTTCGAACACGCTTGA 650
Db |||||
QY 284 CCATGATGCCAGCCACT 301
Db |||||
QY 649 GCAACACGATCTGGTCT 632
Db |||||

RESULT 5
US-11-293-697-965/c
; Sequence 965, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 965
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-965

Query Match 7.8%; Score 33.8; DB 7; Length 2139;
Best Local Similarity 53.4%; Pred. No. 1;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 196 GCCGAGGAGCTGACATGCTCGCCTGAGAGCTGTACAAACAGGGCTTTCGGGGC 255
Db |||||
QY 1422 GCCGGGAGGCGGCTGTAGCTGACAGCAGCTGCAAGGGCCCTGGGTCCCGCC 1363
Db |||||

QY 256 AGCCTCATCAAGCTCGAAGGGCCCTTGACGATGATGGCCAGCAGCACTACAAGCAGCACTGC 315
Db |||||
QY 1362 GGCCCCATCAGCCACAGGGGAGCAGCTGTATGATGCTGCAGGGCCACCTGCAGGGCTGT 1303
Db |||||
QY 316 CCCCCCACCCTGG 328
Db |||||
QY 1302 GTCCCCCTCCTCG 1290
Db |||||

RESULT 6
US-11-293-697-1196/c
; Sequence 1196, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1196
; LENGTH: 2243
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1196

Query Match 7.8%; Score 33.8; DB 7; Length 2243;
Best Local Similarity 53.4%; Pred. No. 1.1;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 196 GCCGAGGAGCTGACATGCTGCAGACTGCCTGAAAGCTGTACAAACAGGGCTTTCGGGGC 255
Db |||||
QY 1527 GCCGGGAGGCGGAGGCTGTAGCTTGACAGCAGCTGCAAGGGCCCTTGGGTCCCCCCC 1468
Db |||||
QY 256 AGCCTCATCAAGCTCGAAGGGCCCTTGACCATGATGGCCAGCAGCACTACAAGCAGCACTGC 315
Db |||||
QY 1467 GGCCCCATCAGCCACCAGGGGAGCAGCTGTATGCTGCAGGGCCACGCTGCAGGGCTGT 1408
Db |||||
QY 316 CCCCCCACCCTGG 328
Db |||||
QY 1407 GTCCCCCTCCTCG 1395
Db |||||

RESULT 7
US-11-293-697-1692/c
; Sequence 1692, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1692
; LENGTH: 2562
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1692

Query Match 7.8%; Score 33.8; DB 7; Length 2562;
Best Local Similarity 53.4%; Pred. No. 1.1;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
QY 196 GCCGAGGAGCTGACATGCTCGCCTGAGAGCTGTACAAACAGGGCTTTCGGGGC 255
Db |||||
QY 1422 GCCGGGAGGCGGCTGTAGCTGACAGCAGCTGCAAGGGCCCTGGGTCCCGCC 1363
Db |||||

Db 1846 GCCGGGAGCCCGAGGCGCTGTAGCTGCAGCAGCAGCTGCAAGGGCCCTGGGTCCCCCCC 1787
QY 256 AGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGGCCACTACAAGCAGCACTGC 315
Db 1786 GSCCCCATCAGCACCAGCGGCGAGCAGCTGATGACGCTGCAGCGCCAGCTGCAGGGCTGT 1727
QY 316 CCCCCCAGCCCTGG 328
Db 1726 GTCCCCCTCCTCG 1714

RESULT 8

US-11-293-697-1541/c
; Sequence 1541, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1541
; LENGTH: 2062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-293-697-1541

Query Match 7.7%; Score 33.6; DB 7; Length 2062;
Best Local Similarity 52.9%; Pred. No. 1.2;
Matches 72; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 190 TTTGAGCGCGAGGAGCTGACATGCCTGCAGACTCGCCTGAAGCTGTACAAACAGGGCTTG 249
Db 189 TTGGAGACTTCCCGCTGTGTCCTGTGTCGATGCGGTGAAGCGTGCAGATGGCTTTG 130
QY 250 CGGGCAGCCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCAGCCACTACAAGCAG 309
Db 129 AGCAGCTCTCTTCAAGCTCCCATGCGCGGCCCTGTGCCCCGCCCAACCCCTCCTG 70
QY 310 CACTGCCCCCCCACCC 325
Db 69 CCCAGCCAGCCCTCC 54

RESULT 9

US-10-953-349-35010
; Sequence 35010, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35010
; LENGTH: 1628
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
US-10-953-349-35010

Query Match 7.7%; Score 33.4; DB 6; Length 1628;
Best Local Similarity 53.4%; Pred. No. 1.2;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 185 AAACCTTTGACCGCCGAGGAGCTGACATGCTGCAGATCGCCTGAAGCTGTACAAACAGG 244

Db 1107 AGACGAACGCGCGCGGAGAGATGTATCAGACGCGCATGCGGAGTACAAGGAGG 1166
QY 245 GCTTGGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCACTACA 304
Db 1167 AGCTGTGGGAGTGCTCTCAAGAAGGAGCAACACCTACTGTATCATGTGCGGGCTCAAGGGCA 1226
QY 305 AGCAGCACTGC 315
Db 1227 TGGAGAGGGC 1237

RESULT 10

US-11-267-871-717
; Sequence 717, Application US/11267871
; Publication No. US20060094655A1
; GENERAL INFORMATION:
; APPLICANT: Guyon, Thierry
; APPLICANT: Borrelly, Gilles
; APPLICANT: Drittanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: MODIFIED GROWTH HORMONES
; FILE REFERENCE: 17109-015001/925
; CURRENT APPLICATION NUMBER: US/11/267,871
; CURRENT FILING DATE: 2005-11-03
; PRIOR APPLICATION NUMBER: 60/706,697
; PRIOR FILING DATE: 2005-08-08
; PRIOR APPLICATION NUMBER: 60/625,652
; PRIOR FILING DATE: 2004-11-04
; NUMBER OF SEQ ID NOS: 719
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717
; LENGTH: 4611
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pTOPO hGH vector
US-11-267-871-717

Query Match 7.5%; Score 32.6; DB 7; Length 4611;
Best Local Similarity 48.2%; Pred. No. 3.1;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
QY 139 AGTGACACTGCTGTATCATGAATGAAACAGTAGAAGTCTCTCTGAAACGTTTCACGCGC 198
Db 2188 AGAAAGCGGCATTTCCACCATGATATTCGGCAAGCAGGATGCCATGGGTACAGAC 2247
QY 199 GAGGAGCTGACATGCTTCAGACTCGCTGAGCTGTACAAACAGGGCTTGGGGGCGAGC 258
Db 2248 GAGATCCTCGCGCTGCGGCATGCTCGCCTTGAGCCTGGGAACAGTTCCGGCTGGCGCGAG 2307
QY 259 CTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCC 318
Db 2308 CCCCTGATGCTCTTCGTCAGATCATCTGTATCGCAAGACCGGCTTCATCCGAGTACG 2367
QY 319 CCCACCTGGA 329
Db 2368 TGCTCGCTCGA 2378

RESULT 11

US-09-484-331-19
; Sequence 19, Application US/09484331
; Publication No. US20060105318A1
; GENERAL INFORMATION:
; APPLICANT: HARRINGTON, JOHN J.
; APPLICANT: SHERF, BRUCE
; APPLICANT: RUNDLETT, STEPHEN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
; TITLE OF INVENTION: ENDOGENOUS GENES
; FILE REFERENCE: 0221-0003L
; CURRENT APPLICATION NUMBER: US/09/484,331
; CURRENT FILING DATE: 2000-01-18
; PRIOR APPLICATION NUMBER: 09/276,820


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RESULT 13
US-10-485-397-10/c
; Sequence 10, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTANA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B697USPCT01
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 5264
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pSEAPstopneo is a circular plasmid DNA
US-10-485-397-10

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RESULT 14
US-09-484-331-27
Sequence 27, Application US/09484331
Publication No. US20060105318A1
GENERAL INFORMATION:
APPLICANT: HARRINGTON, JOHN J.
APPLICANT: SHERP, BRUCE
APPLICANT: RUNDETT, STEPHEN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NON-TARGETED ACTIVATION OF
TITLE OF INVENTION: ENDOGENOUS GENES
FILE REFERENCE: 0221-0003L
CURRENT APPLICATION NUMBER: US/09/484,331
CURRENT FILING DATE: 2000-01-18
PRIOR APPLICATION NUMBER: 09/276,820
PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 09/263,814
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: 09/253,022
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/159,643
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 08/941,223
; PRIOR FILING DATE: 1997-09-26
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 5314
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-484-331-27

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Best Local Similarity 48.2%; Pred. No. 3.3;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
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Db |||||
Db 2329 AGAAAGCGGCCATTTCCACCATGATATTCGGCAAGCAGGCATGCCCATGGGTCCAGAC 2388
QY 199 GAGGAGCTGACATGCTCGAGACTCGCCTGAAGCTGTACAAACAGGGCTTCGGGGGCAGC 258
Db |||||
Db 2389 GAGATCCTCGCGTCGGGCATGCTCGCCTTGAGCCTTGGCGAACAGTTTCGGCTGGCGCGAG 2448
QY 259 CTCATCAAGCTCGAAGGCCCTTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCCC 318
Db |||||
Db 2449 CCCCTGATGCTCTTCGTCAGATCATCTCGATCGACAGACCGGCTTCCATCCGAGTAGC 2508
QY 319 CCCACCCCTGGA 329
Db |||||
Db 2509 TGCTCGCTCGA 2519

RESULT 15

US-10-485-397-9/c
; Sequence 9, Application US/10485397
; Publication No. US20060099673A1
; GENERAL INFORMATION:
; APPLICANT: ALTANA Pharma AG
; TITLE OF INVENTION: Novel Recombinant Gene Expression Method
; FILE REFERENCE: B69/USPTO1
; CURRENT APPLICATION NUMBER: US/10/485,397
; CURRENT FILING DATE: 2004-01-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 5408
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: pSEAPstopMneo is a circular Plasmid DNA
US-10-485-397-9

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Best Local Similarity 48.2%; Pred. No. 3.3;
Matches 92; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
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Db |||||
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QY 199 GAGGAGCTGACATGCTCGAGACTCGCCTGAAGCTGTACAAACAGGGCTTCGGGGGCAGC 258
Db |||||
Db 2824 GAGATCCTCGCGTCGGGCATGCTCGCCTTGAGCCTTGGCGAACAGTTTCGGCTGGCGCGAG 2765
QY 259 CTCATCAAGCTCGAAGGCCCTTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCCC 318
Db |||||
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QY 319 CCCACCCCTGGA 329
Db 2704 TGCTCGCTCGA 2694
Search completed: May 26, 2006, 01:31:24
Job time : 133 secs

GenCore version 5.1.8

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 00:46:33 ; Search time 3394 Seconds
(without alignments)
7167.033 Million cell updates/sec

Title: US-10-614-481-8

Perfect score: 435

Sequence: 1 atgtggctgcagaactgtct.....ggaagccagccaggaagtaa 435

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 2795965780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est3:*

3: gb_est4:*

4: gb_est5:*

5: gb_est6:*

6: gb_hic:*

7: gb_est2:*

8: gb_est7:*

9: gb_est8:*

10: gb_est9:*

11: gb_gss1:*

12: gb_gss2:*

13: gb_gss3:*

14: gb_gss4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	331	76.1	435	14	DQ053415	DQ053415 Homo sapi
2	331	76.1	588	7	AW207707	AW207707 UI-H-BI2-
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4	331	76.1	666	1	AI912784	AI912784 wel3f07.x
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8	329.4	75.7	584	5	CF341802	CF341802 TgESTzyj4
9	329	75.6	895	7	BE873976	BE873976 601484045
10	323	74.3	585	5	CF370833	CF370833 TgESTzyj5
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c 21	272.2	62.6	701	3	BU633411	BU633411 UI-H-FL1-
c 22	271	62.3	475	1	AA995402	AA995402 or74f05.a
c 23	264.8	60.9	388	10	DV799573	DV799573 est.t.tru
c 24	258	59.3	666	4	CA307828	CA307828 UI-H-FT1-
c 25	244.2	56.1	661	5	CD368851	CD368851 UI-H-FT1-
c 26	233.6	53.7	336	7	AW951121	AW951121 EST363191
c 27	219.8	50.5	1034	6	AK053196	AK053196 Mus muscu
c 28	208.8	48.0	608	5	CD367244	CD367244 UI-H-FT2-
c 29	183.6	42.2	549	1	AI677936	AI677936 wc88f12.x
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c 31	179.8	41.3	629	7	BB664267	BB664267 BB664267
c 32	176.2	40.5	531	2	BG236310	BG236310 naf26a07.
c 33	167.8	38.6	631	9	DN753142	DN753142 GL-CF-993
c 34	149.6	34.4	647	7	BB533718	BB533718 BB533718
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c 37	134.2	30.9	517	4	CB430980	CB430980 606916 MA
c 38	123	28.3	483	1	AI180659	AI180659 uc47d08.x
c 39	122.4	28.1	369	4	BX521029	BX521029 BX521029
c 40	112.8	25.9	470	1	AI121878	AI121878 ud13e11.x
c 41	108	24.8	488	9	DN505558	DN505558 HL01015B1
c 42	106.2	24.4	697	14	AG112609	AG112609 Pan trogl
c 43	103	23.7	678	9	DR004241	DR004241 TC124014
c 44	96	22.1	160	5	CF341980	CF341980 TgESTzyj5
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ALIGNMENTS

RESULT 1	DQ053415	435 bp	DNA	linear	GSS 02-JUN-2005
DQ053415	Homo sapiens	HC14003 gene, VIRTUAL TRANSCRIPT, partial sequence,			
LOCUS	DQ053415	genomic survey sequence.			
DEFINITION	DQ053415.1	GI:66899362			
ACCESSION	DQ053415				
VERSION	GSS				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 435)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees				
JOURNAL	(er) PLoS Biol. 3 (6), E170 (2005)				
PUBMED	15869325				
REFERENCE	2 (bases 1 to 435)				
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fedel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.				
TITLE	Direct Submision				
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.				
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gene					
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Query Match	76.1%	Score 331	DB 14	Length 435	

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DEFINITION	similar to gb:M1220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN);, mRNA sequence.				
ACCESSION	BE218982				
VERSION	BE218982.1	GI:8906300			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 660)				
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: rgapbs-r@mail.nih.gov Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov Seq primer: -40UP from Gibco High quality sequence stop: 445. Location/Qualifiers 1. .660 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:3176532" /tissue_type="carcinoid" /lab_host="DH10B" /clone_lib="NCI CGAP Lu24" /notes="Organ: lung; Vector: p77T3D-PacI; Plasmid DNA from the normalized library NCI_CGAP_Lus was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."				
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ORIGIN					
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QY	121	AGCCTTCTGAACAACACTAGTGCACCTGTCTATCATGAATGAACAGTAGAAGTCGTC	180		
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QY	181	TCTGAAACGTTTGAACGCCAGGAGCTGACATGCCTGCAGACTCGCTGGAAGCTGTACAA	240		
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the normalized library NCI CGAP Lu5 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo."
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  Query Match      76.1%; Score 331; DB 7; Length 695;
  Best Local Similarity 85.1%; Pred. No. 6.6e-83;
  Matches 370; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
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  DB 41 ATGTGGCTGCAGAGCCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 100
  QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGGAGCATGTGGATGCCATCAAGAGGCCCTTG 120
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  QY 121 AGCCTTCTGAACACAGTAGTGACACTGCTATCATGAATGAACAGTAGTAAGTCGTC 180
  DB 161 CGTCTCTCTGAACCTGAGTAGAGACTGCTGCTGAGATGAATGAACAGTAGTAAGTCATC 220
  QY 181 TCTGAAACGTTTGACCGCGAGAGCTGACATGCTCTGCAGACTCGCCTGAAGCTGTACAA 240
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  QY 241 CAGGCTTGGGGGAGCCTCATCAAGCTGAGGCCCTTGAACCATGATGCCAGCCAC 300
  DB 281 CAGGCTTGGGGGAGCCTCACCAGCTCAAGGCCCTTGAACCATGATGCCAGCCAC 340
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  QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAAG 420
  DB 401 GAAAGTTTCAAGAGAACTGAAGGACTTTCTGTGTTGATCCCTTTGACTGTGGAG 460
  QY 421 CCAGCCCAAGAGTAA 435
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    genomic survey sequence.
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    DQ053416
  VERSION
    DQ053416.1 GI:66899363
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    GSS.
  SOURCE
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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  REFERENCE
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    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
    Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
    White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
    A Scan for Positively Selected Genes in the Genomes of Humans and
    Chimpanzees
    (er) PLOS Biol. 3 (6), E170 (2005)
    15869325
    2 (bases 1 to 435)
    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
    Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civeello,D.,
    White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
    Direct Submission
    Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
    Rockville, MD 20850, USA
    This sequence was made by sequencing genomic exons and ordering
    them based on alignment. Translation starts at the beginning of
    alignment.
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  QY 61 CGCCAAACCCAGCCCTGTCACTCGGCCCTGGGAGCATGTGGATGCCATCAAGAGGCCCTTG 120
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Qy	363	AAGTTTCAAAAAGAACCTGGAAGGATTTTCTGTTTCAGATGCCGTTTGACTGCTGGAAGCC	422
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Qy	423	AGCCCCAGAAATGA	435
Db	421	AGTCCAGAGTGA	433
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CF370833			
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	cDNA clone TgESTzyJ5se12.y1 5', similar to SW:CSF2 HUMAN P04141		
	GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR		mRNA
	sequence.		

CF370833 585 bp mRNA linear EST 27-AUG-2003
 LOCUS TgESTzyJ55e12.y1 Tg CAST Tachyzoite cDNA library Toxoplasma gondii
 DEFINITION cDNA clone TgESTzyJ55e12.y1 5' similar to SW:CSF2 HUMAN P04141
 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
 sequence.

the fragments were digested with SfiI. The fragments were size selected, ligated into a modified pBluescript vector (obtained from Michael White, Montana State University) containing directional SfiI sites, and electroporated into ElectroGen Blue cells. Vector: SfiI sites were added to the multiple cloning region of pBluescript SK+ between the BamHI/NotRI sites. The modified polylinker has the following sequence: 5'GAATTCGGCATTCAGGCC(G)n- insert--GCCCGCTTCGCCACGATCTC3' where n=3-4 G nucleotides..

WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University"

ORIGIN

Query Match	74.3%;	Score 323;	DB 5;	Length 585;
Best Local Similarity	83.9%;	Pred. No. 1.2e-80;		
Matches 365;	Conservative 0;	Mismatches 70;	Indels 0;	Gaps 0;

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QY	61	CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120
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QY	121	AGCCTTCTGAACAACAGTAGTGACACTGCTGCTCTATCATGAATCAAAACAGTAGAAGTCTGTC	180
DB	155	CGTCTCTGAACTGTGAGTAGAGACACTGCTGCTGAGATGATTTATAGTAGAAGTCATC	214
QY	181	TTCTGAAACGTTTGACGCCGAGGAGCTGACATGCTCGAGACTCGCCTGGAAGCTGTACAAA	240
DB	215	TCAGAAATGTTTGACCTCCAGGAGCGCATCTGCTACAGACCCGCCCTGGAGCTGTACAA	274
QY	241	CAGGGCTTCGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCAC	300
DB	275	CAGGGCTTCGGGGGAGCCCCACCAAGCTCAAGGGGCCCTTGACCATGATGGCCAGCCAC	334
QY	301	TACAAGCAGCACTGCCCCCCCCACCCTTGGAAACTTCTCTGTGCAACCCAGATGATCACTTC	360
DB	335	TACAAGCAGCACTGCCCCCTCAACCCCGGAAACTTCTCTGTGCAACCCAGCATATCACCTTT	394
QY	361	AAAAAGTTTCAAAAGAACTGGAAGGATTTTCTGTTTGGATCCCGTTTGACTCTCTGGAAG	420
DB	395	GAAAGTTTCAAGAGAACTGAAGGACTTCTGCTGTCTATCCCTTGTACTCTCTGGGAG	454
QY	421	CCAGCCCCAAGATTA	435
DB	455	CCAGTCCAGAGTGA	469

RESULT 11

CF370966	592 bp	mRNA	linear	EST 27-AUG-2003
TGESTzy158e12.y1 Tg CAST Tachyzoite cDNA Library				Toxoplasma gondii
cDNA clone TGESTzy158e12.y1 5' similar to SW:CSF2.HUMAN.P04141				
GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;				mRNA
sequence.				
CF370965				
CF370966.1	GI:34318212			
EST.				
Toxoplasma gondii				
Toxoplasma gondii				
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;				
Sarcocystidae; Toxoplasma.				
1 (bases 1 to 592)				
Tang, K., Cole, R., Fogarty, S., Sibley, L. D., Ajioka, J. A., White, M.,				
Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,				
Hillier, L., Kucaba, T., Theising, B., Bowers, F., Gibbons, M.,				
Ritter, E., Bennett, J., Franklin, C., Tsagarisshvili, R., Ronko, I.,				
Kennedy, S., Maguire, L., Waterston, R. and Wilson, R.				
Toxoplasma EST Project				
Unpublished (2001)				
TITLE				
JOURNAL				

COMMENT

Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxoes@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
Seq primer: -40UP from Gibco.

FEATURES

source

1..592
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="TgESTyJ5812.y1"
/dev_stage="Tachyzoite"
/lab_host="ElectroTen Blue cells (Stratagene)"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/note="Vector: Modified pBluescript (pBS SK+); Site 1:
BamHI; Site 2: EcoRI; The cDNA library was constructed by
Kellang Tang, and Robert Cole at Washington University.
cDNA was synthesized from poly(A) + mRNA using the
template-switching PCR method (SMART cDNA Kit, BD
Biosciences). First strand cDNA was reverse transcribed
using the CDS III/3' primer and a 5' template switch
primer (Smart IV primer). The product of the first strand
synthesis was PCR amplified using the same primer set and
the fragments were digested with SfiI. The fragments were
size selected, ligated into a modified pBluescript vector
(obtained from Michael White, Montana State University)
containing directional SfiI sites, and electroporated into
ElectroTen Blue cells. Vector: SfiI sites were added to
the multiple cloning region of pBluescript SK+ between the
BamHI/EcoRI sites. The modified polylinker has the
following sequence: 5'GAATTCGGCATTCAGGCC(G)n-- insert--
GGCGCCTCGGCACGATCC3' where n=3-4 G nucleotides.
WARNING: the library contains a small percentage of cDNAs
derived from the human host cells. Library materials
provided by David Sibley, Washington University."

ORIGIN

Query Match 74.3%; Score 323; DB 5; Length 592;
Best Local Similarity 83.9%; Pred. No. 1.2e-80;
Matches 365; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGATCCCGCACCCACC 60
DB 35 ATGTGGATGCAGAGCTGCTGCTCTTGGGCACTGTGGCTGCAGCATCTCTGCACCCGCC 94

QY 61 CGCCAAACCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGCCCTTG 120
DB 95 CGCTCGCCAGCCCGCAGCAGCCGCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 154

QY 121 AGCCTTCTGAACACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGTAAGTCGTC 180
DB 155 CGTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGATAGTAGATCATC 214

QY 181 TCTGAACGCTTTGACGCCGAGAGCTGACATGCCCTGCAGACTCGCCTGAAGCTGTACAAA 240
DB 215 TCAGAAATGTTTGACCTCCAGAGCGCGACCTGCTCTACAGACCCGCTGGAGCTGTACAAG 274

QY 241 CAGGCTTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTTGACCATGATGCCAGCCAC 300
DB 275 CAGGCTTTCGGGGGAGCCCGCACCAAGCTCAAGGCCCTTTGACCATGATGCCAGCCAC 334

QY 301 TACAGAGACACTGCCCCCGCCACCTCGAAACTCTCTGTGCAACCCAGATGATCACTTC 360
DB 335 TACAGAGACACTGCCCCCTCCAAACCCCGGAACTCTCTGTGCAACCCAGACTATCACTTT 394

QY 361 AAAAGTTTCAAAAAGAACTGAAGGATTTTCTGTTTGAGATCCCGCTTTGACTGTGGAG 420
DB 395 GAAAGTTTCAAAAGAACTGAAGGACTTTCTGCTTGTCATCCCTTTGACTGTGGAG 454

QY 421 CCAGCCCCAGAGTAA 435
DB 455 CCAGTCCAGGAGTGA 469

RESULT 12
BX111836/c
LOCUS BX111836 NCI_CGAP Lu5 Homo sapiens cDNA clone IMAGE9998C104061 ;
DEFINITION IMAGE:1601601, mRNA sequence.
ACCESSION BX111836
VERSION BX111836
KEYWORDS BX111836.1 GI:27837278
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 658)
AUTHORS Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U., Schneider,B. and Korn,B.
TITLE Human Unigeneset - RZPD3
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGE9998C104061.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Human Unigeneset - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/cgi-
bin/showlib.pl.cgi?response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGAAACACGCTATGAC.

FEATURES
source
1..658
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE9998C104061 ; IMAGE:1601601"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Lu5"
/note="Organ: lung; Vector: pTV73D-PacI; 1st strand cDNA
was prepared from neuroendocrine lung carcinoid, and was
then primed with a Not I - oligo(dT) primer.
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pTV73 vector. Library is
normalized. Library was constructed by Bento Soares and M.
Fatima Bonaldo."

ORIGIN
Query Match 73.3%; Score 319; DB 4; Length 658;
Best Local Similarity 84.6%; Pred. No. 1.7e-79;
Matches 358; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 13 AACCTGCTTCTTCTGGGCACTGTGGTTTACAGATCCCGCACCCACCCGCCAACCCAGC 72
DB 658 AGCCTGCTGCTTCTGGGCACTGTGGCTTGCAGCATCTCTGCACCCCGCTCGCCCCAG 599

QY 73 CCTGTCACTCGGCCCTGCAGCATGTGGATGCATCAAGGAGGCCCTGAGCCTTCTGAAC 132
DB 598 CCGACACGACGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCTCTCTGAAC 539

QY 133 AACAGTAGTGAACCTGCTGCTATCATGAATGAACAGTAGAAGTCGTCTCTGAACGTTT 192

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Db      538 CTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGTAAGTCAATCTCAGAAAATGTTT 479
QY      193 GACGCGGAGGAGCTGACATGCGCTGCAGACTCGCCTGAAGCTGTACAAAACAGGGCTTGCGG 252
Db      478 GACCTCCAGGAGCCGACCTGCTACAGACCCGCTGGAGCTGTACAGCAGGGCTTGCGG 419
QY      253 GCAGGCTCATCAAGCTCGAAGGCCCTTTCATGATGCGCAGGCACATACAAAGCAGCAC 312
Db      418 GCGAGCTCACCAAGCTCAAGGGCCCTTTCAGCATGATGCGCAGGCACATACAAAGCAGCAC 359
QY      313 TGCSCCCCCACCTCGAACTTCCTGTGCAACCCAGATGATCACTTCAAAAGTTTCAA 372
Db      358 TCCCTTCCAAACCCCGAAATTCCTGTGCAACCCAGATTCACCTTTGAAAAGTTTCAA 299
QY      373 AAGAACTTGAAGGATTTCTGTTTGAGATCCCGTTTGACTGTGGAAGCCAGCCAGAG 432
Db      298 GAGAACTTGAAGGACTTCTGCTTGTCTATCCCTTTCAGCTGTGGAGGCACTCCAGGAG 239
QY      433 TAA 435
Db      238 TGA 236

RESULT 13
LOCUS      CB457551
DEFINITION 714908 MARC 6BOV Bos taurus cDNA 5', mRNA linear EST 26-MAR-2003
ACCESSION  CB457551
VERSION     CB457551.1 GI:29263933
KEYWORDS    EST.
SOURCE      Bos taurus (cattle)
ORGANISM    Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1 (bases 1 to 561)
AUTHORS     Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
            Wray,J.E. and Keale,J.W.
TITLE       A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL     Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel.: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: FQY8072 row: H column: 12
            Seq primer: GTAATACGACTCATTATAGG.
FEATURES    Location/Qualifiers
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                        /tissue_type="pooled"
                        /lab_host="DH10B"
                        /clone_lib="MARC 6BOV"
                        /note="Vector: pDON3.1; Site 1: EcoRI; Site 2: NotI;
                        Library made with RNA pooled from multiple tissues
                        including liver, lung, hypothalamus, pituitary, and
                        placenta/endometrium."

ORIGIN
Query Match 73.1%; Score 318.2; DB 4; Length 561;
Best Local Similarity 84.8%; Pred. No. 2.7e-79;
Matches 369; Conservative 0; Mismatches 63; Indels 3; Gaps 1;

QY      1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGGTTTACAGCATGCCGCGACCCACC 60
Db      17 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGGTCTGCAGCTTCTCCGCACTACT 76

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QY      61 CGCCAAACCCAGCCCTGTCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 120
Db      77 CGCCCAACCCAACTGCGCCACCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTTG 136
QY      121 AGCCTTCTGACCAACAGTAGTACACTGCTGCTATCATGAATGAACAGTAGTAAGTCTGTC 180
Db      137 AGCCTTCTGAAACACAGCAGTAGTACACTGATGCTGTGTAATGACAC---AGAAGTCGTC 193
QY      181 TCTGAAAAGCTTTGACCGCGGAGGAGCTGACATGCTCTGCAGACTCGCTGAAGCTGTACAAA 240
Db      194 TCTGAAAAGTTTGACTCCAGGAACCAAGCTGCTGCAGACTCGCTGAAGCTGTACAAAG 253
QY      241 CAGGCTTGGGGGAGAGCTCATCAAGCTGCAAGGCCCTTCAGCATGATGCCAGCCAC 300
Db      254 AACGCTTGCAGGGCAGGCTCACTAGTCTCATGCGGCTCTTGACCATGATGCCACCCAC 313
QY      301 TACAGCAGCACTGCCCCCCCCACCTGGAATCTTCTGTGCAACCCAGATGATCACTTTC 360
Db      314 TACGAGAAACACTGCCCCACCCACCCCGGAACTTCTCTGTGGAACCCAGTTTATCATGCTTC 373
QY      361 AAAAGTTTCAAAAAGAACTGAAGGATTTCTGTTTGAGATCCCTTTGACTGCTGGAAAG 420
Db      374 AAAAATTTCAAGAGGAGCTGAAGGAGTTCTTTTATCATTCCTTTGACTGCTGGGAA 433
QY      421 CCAGCCCAAGATGA 435
Db      434 CCAGCCCAAGATGA 448

RESULT 14
LOCUS      BM539160
DEFINITION hb05e10.g1 Canis cDNAs from testes cells Canis familiaris cDNA
            clone hb05e10 5', mRNA sequence.
ACCESSION  BM539160
VERSION     BM539160.1 GI:18820855
KEYWORDS    EST.
SOURCE      Canis familiaris (dog)
ORGANISM    Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
            Canis.
REFERENCE   1 (bases 1 to 572)
AUTHORS     O'Shaughnessy,A.L., McCombie,W.R., Baker,J.P., Balija,V.,
            Cunnius,D., Dedhia,N.N., de la Bastide,M., Katzenberger,F.,
            King,L., Kirchoff,K.A., Miller,B., Muller,S., Nascimento,L.U.,
            Palmer,L., Santos,L., Shah,R.S., Spiegel,L.A., Zutavern,T.,
            Preston,R. and Hannon,G.J.
            Expressed sequence tags from Canis familiaris (dog) (2002)
            Unpublished (2002)
            Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mcombie@cshl.org
            Plate: hb05 row: e column: 10
            Seq primer: -21M13UnivRev
            High quality sequence stop: 572.
FEATURES    Location/Qualifiers
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                        /organism="Canis familiaris"
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                        /clone_lib="hb05e10"
                        /tissue_type="testes"
                        /note="Vector: Lambda Zap II; The library was produced by
                        Greg Hannon and Raymond Preston (Cold Spring Harbor
                        Laboratory). This library is oligo(dT) primed using
                        stratagene zap cDNA synthesis kit. It was made from dog
                        testes. Please contact Greg Hannon (hannon@cshl.org) with

```

ORIGIN		any library related inquiries."	
Query Match		73.1%; Score 318.2; DB 2; Length 572;	
Best Local Similarity		83.2%; Pred. No. 2.8e-79;	
Matches 362; Conservative 0; Mismatches 73; Indels 0; Gaps 0;			
Qy	1	ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGGATCCCGCAGCCACC	60
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Qy	61	CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120
Db	89	CGCTCACCACCCCTTGTCTCACTCGGCCCTCTCAGCACGTGGATGCCATCCAGGAGCCCTG	148
Qy	121	AGCCTTCTGAACAAACAGTAGTACACTGCTGCTATCATGAATGAACAGTAGTAAGTGTCTC	180
Db	149	AGCCTTTTGAACAAACAGTAATGACGTGCTGTGATGAATAAAGCAGTAAGAGTGTCTC	208
Qy	181	TCTGAACGTTTGAAGCCGAGAGAGCTGACATGCTCTGAGACTCGGCTGAAGCTGTACAAA	240
Db	209	TCTGAAGTGTTTGACCTTGAGGGGCCAACATGCTCTGGAGACCCGCTTACAGCTGTACAA	268
Qy	241	CAGGCTTTCGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC	300
Db	269	GAGGCTTCGACGGGAGCCTCACACGCTCAAGACCTCAAGAAATCCCTTAAACATGATGCC	328
Qy	301	TACAGCAGCAGCTGCCCCCCCCCAGCTTCTGTGCAAACTTCTGTGCAACCCAGATGATCA	360
Db	329	TATAAGCAGCAGCTGCCCCCTACCCCGGAATCTCCCTGTGCAACCCAGAAATTAATTC	388
Qy	361	AAAAGTTTCAAAAGAACCTGAAGATTTCTGTTTGATGATCCGTTTGTGCTGGAAG	420
Db	389	AAAAGTTTCAAAAGAACCTGAAGATTTCTGTTTAAATCATCCCTTTGACTGTGGA	448
Qy	421	CCAGCCCAAGTAA	435
Db	449	CCAGTCAAGAAGTGA	463
RESULT 15		CF614774 672 bp mRNA linear EST 01-OCT-2003	
LOCUS		CES009198 Bos taurus muscle cDNA library Bos taurus cDNA clone	
DEFINITION		CCL009198 5', mRNA sequence.	
ACCESSION		CF614774	
VERSION		CF614774.1 GI:37240821	
KEYWORDS		EST.	
SOURCE		Bos taurus (cattle)	
ORGANISM		Bos taurus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.	
AUTHORS		Wang,Y.H., Byrne,K.A., Reverter,A., Harper,G.S., Taniguchi,M., McWilliam,S.M., Mannen,H., Oyama,K. and Lehnert,S.A.	
TITLE		Transcriptional profiling of skeletal muscle tissue from two breeds of cattle	
JOURNAL		Mamm. Genome 16 (3), 201-210 (2005)	
PUBMED		15834637	
COMMENT		Contact: Dr Sigrid Lehnert Functional Genomics Lab CSIRO Livestock Industries Level 5, Queensland Bioscience Precinct, University of Queensland, 306 Carmody Road St.Lucia QLD Australia Tel: 07 3214 2445 Fax: 07 3214 2480 Email: Sigrid.Lehnert@csiro.au Plate: 08 row: D column: 01. Location/Qualifiers 1..672 /organism="Bos taurus" /mol_type="mRNA"	

Search completed: May 26, 2006, 03:43:10
Job time : 3398 secs

ORIGIN		/strain="Angus" /db_xref="taxon:9913" /clone="CCL009198" /sex="male" /tissue_type="Longissimus dorsi muscle" /dev_stage="Young Adult" /lab_host="XLI-BlueMRF'strain" /clone_lib="Bos taurus muscle cDNA library" /note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site_1: EcoRI; Site_2: Xho I; Library made from skeletal muscle of a 14 month old Angus steer."	
Query Match		72.5%; Score 315.2; DB 5; Length 672;	
Best Local Similarity		84.1%; Pred. No. 2.1e-78;	
Matches 366; Conservative 0; Mismatches 66; Indels 3; Gaps 1;			
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Db	19	ATGTGGNNAGAACCTGCTTCTCTGGGCACTGTGGTCTGCAGCTTCTCCGCACCTACT	78
Qy	61	CGCCAAACCCAGCCCTGTCACCTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120
Db	79	CGCCACCCAAACACTGCCACCCGCGCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	138
Qy	121	AGCCTTCTGAACAAACAGTAGTGACACTGCTCTCATCATGAATGAACAGTAGTAGTCGTC	180
Db	139	AGCCTTCTGAACCCACAGCAGTGACACTGATGCTGTGATGAATGACAC---AGAAATCGTC	195
Qy	181	TCTGAACGTTTGAACGCGCGAGGAGCTGACATGCTCTGCAGACTCGCCTGAAGCTGTACAAA	240
Db	196	TCTGAAGAATTTGACTCCAGGAAACCAACGTCGCTGCAGACTCGCCTGAAGCTGTACAA	255
Qy	241	CAGGCTTTCGCGGCGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC	300
Db	256	AACGCGCTGCAGGGCAGCCTCACTAGTCTCATGGGCTCTTGACCATGATGCCACCCAC	315
Qy	301	TACAGCAGCAGTCCCCCCCCCAGCTTCTGTGGAACCTTCTGTGGAACCCAGATGATCACCTTC	360
Db	316	TACGAGAAACACTGCCACCCACCCCGGAAACTTCTCTGTGGAACCCAGTTTATCAGCTTC	375
Qy	361	AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGTGCTGGAAG	420
Db	376	AAAATTTCAAGAGGAGCTGAAGGAGTTCTTTTATCATTCCTTTGACTGTCTGGGAA	435
Qy	421	CCAGCCCAAGTAA	435
Db	436	CCAGCCCAAGTGA	450

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 01:01:29 ; Search time 164 Seconds
(without alignments)
4963.002 Million cell updates/sec

Title: US-10-614-481-8

Perfect score: 435

Sequence: 1 atgtggctgcagaacctgt.....ggaagccagccagagtaa 435

Scoring table: IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- Issued Patents NA:*
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 - 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 - 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 - 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	435	100.0	435	3	US-09-589-460-8	Sequence 8, Appli
2	332.6	76.5	444	3	US-09-322-409-119	Sequence 119, App
3	332.6	76.5	444	3	US-09-322-409-121	Sequence 121, App
c	332.6	76.5	444	3	US-09-451-527-119	Sequence 119, App
4	332.6	76.5	444	3	US-09-451-527-121	Sequence 121, App
5	332.6	76.5	444	5	US-10-262-439-119	Sequence 119, App
6	332.6	76.5	444	5	US-10-262-439-121	Sequence 121, App
c	332.6	76.5	444	5	US-10-262-439-121	Sequence 121, App
7	332.6	76.5	798	2	US-08-133-979A-10	Sequence 10, Appl
8	332.6	76.5	798	2	US-08-436-890-10	Sequence 10, Appl
9	332.6	76.5	798	2	US-08-451-213-10	Sequence 10, Appl
10	332.6	76.5	798	2	US-08-451-213-10	Sequence 9, Appli
11	331.2	76.1	432	3	US-09-617-594A-9	Sequence 9, Appli
12	331.2	76.1	432	3	US-10-209-507-9	Sequence 8, Appli
13	331	76.1	435	3	US-08-848-760B-8	Sequence 8, Appli
14	331	76.1	435	3	US-09-826-025-8	Sequence 8, Appli
15	331	76.1	789	5	US-09-543-679A-2706	Sequence 2706, Ap
16	331	76.1	5115	5	US-09-543-679A-2709	Sequence 2709, Ap
17	329.6	75.8	432	3	US-09-322-409-122	Sequence 122, App
c	329.6	75.8	432	3	US-09-322-409-123	Sequence 123, App
18	329.6	75.8	432	3	US-09-451-527-122	Sequence 122, App
19	329.6	75.8	432	3	US-09-451-527-123	Sequence 123, App
c	329.6	75.8	432	3	US-09-451-527-123	Sequence 123, App
20	329.6	75.8	432	3	US-09-617-594A-7	Sequence 7, Appli
21	329.6	75.8	432	3	US-10-209-507-7	Sequence 7, Appli
22	329.6	75.8	432	3	US-10-209-507-7	Sequence 7, Appli
23	329.6	75.8	432	5	US-10-262-439-122	Sequence 122, App

C	24	329.6	75.8	432	5	US-10-262-439-123	Sequence 123, App
	25	329.6	75.8	1032	3	US-09-555-165-8	Sequence 8, Appli
	26	329.6	75.8	1032	3	US-09-555-165-10	Sequence 10, Appl
	27	329.4	75.7	435	3	US-10-188-056-32	Sequence 32, Appl
	28	329.4	75.7	496	2	US-08-184-009-191	Sequence 191, App
	29	329.4	75.7	496	2	US-08-458-356-191	Sequence 191, App
	30	329.4	75.7	496	3	US-08-460-736-191	Sequence 191, App
	31	329.4	75.7	496	3	US-09-535-370-191	Sequence 191, App
	32	329.4	75.7	496	3	US-09-663-667-191	Sequence 191, App
	33	329.4	75.7	756	3	US-09-016-434-1195	Sequence 1195, Ap
	34	329.4	75.7	1318	3	US-09-310-842-3	Sequence 3, Appli
	35	328	75.4	945	2	US-08-750-128-7	Sequence 7, Appli
	36	327.8	75.4	435	3	US-10-188-056-34	Sequence 34, Appl
	37	326.4	75.0	969	2	US-08-750-128-4	Sequence 4, Appli
	38	318.2	73.1	809	2	US-08-259-696B-6	Sequence 6, Appli
	39	318.2	73.1	809	2	US-08-259-696B-8	Sequence 8, Appli
	40	318.2	73.1	809	2	US-08-902-513-6	Sequence 6, Appli
	41	318.2	73.1	809	2	US-08-902-513-8	Sequence 8, Appli
	42	315	72.4	1011	3	US-09-976-594-275	Sequence 275, App
	43	301.6	69.3	660	10	5391485-2	Patent No. 5391485
	44	301.6	69.3	661	10	5229496-1	Patent No. 5229496
	45	296.4	68.1	1588	2	US-09-146-283-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-589-460-8
; Sequence 8, Application US/09589460
; Patent No. 6645740
; GENERAL INFORMATION:
; APPLICANT: Bublout, et al.
; TITLE OF INVENTION: Equine GM-CSF
; FILE REFERENCE: 454313-2334.1
; CURRENT APPLICATION NUMBER: US/09/589,460
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/138,843
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Equine sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(432)
; OTHER INFORMATION: coding sequence of equine GM-CSF gene
US-09-589-460-8

Query Match	100.0%	Score 435;	DB 3;	Length 435;
Best Local Similarity	100.0%	Pred. No. 5.2e-118;	Mismatches 0;	Indels 0;
Matches 435;	Conservative 0;			Gaps 0;
QY	1	ATGTGGCTGCAGAACCTGCTCTCTCTGGGCACCTGTGGTGTACAGCATGCCCGACCCACC	60	
Db	1	ATGTGGCTGCAGAACCTGCTCTCTCTGGGCACCTGTGGTGTACAGCATGCCCGACCCACC	60	
QY	61	CGCCCAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120	
Db	61	CGCCCAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120	
QY	121	AGCCTTCTGAAACAAACAGTAGTACACTGCTGTATCATGAATGAAACAGTAGAAGTCGTC	180	
Db	121	AGCCTTCTGAAACAAACAGTAGTACACTGCTGTATCATGAATGAAACAGTAGAAGTCGTC	180	
QY	181	TCTGAAACCTTTGACGCCCGAGGAGCTGACATGCCCTGCAGACTCGCCTGAAGCTGTACAA	240	
Db	181	TCTGAAACCTTTGACGCCCGAGGAGCTGACATGCCCTGCAGACTCGCCTGAAGCTGTACAA	240	
QY	241	CAGGGCTTCGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTACACCATGATGCCAGCCAC	300	

Db 241 CAGGCTTGGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
QY 301 TACAAGCAGCACTGCCCCCACTTGGAAATCTCTGTGCAACCCAGATGATCACTTC 360
Db 301 TACAAGCAGCACTGCCCCCACTTGGAAATCTCTGTGCAACCCAGATGATCACTTC 360
QY 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
Db 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
QY 421 CCAGCCCAAGATAA 435
Db 421 CCAGCCCAAGATAA 435

RESULT 2
US-09-322-409-119
; Sequence 119, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus

Query Match 76.5%; Score 332.6; DB 3; Length 444;
Best Local Similarity 85.3%; Pred. No. 6.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGCATGCCGACCCACC 60
Db 10 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGCATGCCGACCCACC 69
QY 61 CGCCAAACCAGCCCTGTCTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db 70 AGTTCAACCAGCTGTCTCACTCGGCCCTGGCAACAGCTGGATGCCATCAAGAGGCCCTG 129
QY 121 AGCCCTTCTGAACAACAGTAGTGACATGCTGTATCATGAATGAACAGTAGAGTCGTC 180
Db 130 AGCCCTTCTGAACAACAGTAGTGAAATACTGCTGTGATGAATGAACAGTAGAGTCGTC 189
QY 181 TCTGAAACGTTTGAAGCCGAGGAGTGACATGCCTGCAGACTCGCCTGAAGCTGTACAA 240
Db 190 TCTGAAATGTTTGACCTTGAGGCGGAAATGCCTGCAGACTCACCTAAAGCTGTAGGAG 249
QY 241 CAGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 250 CAGGCTTACGGGAGCCCTCATCAAGCTCAAGGAGCCCTCTGAGAATGATGCCAACCAT 309
QY 301 TACAAGCAGCACTGCCCCCACTTGGAAATCTCTGTGCAACCCAGATGATCACTTC 360
Db 310 TACAAGCAGCACTGCCCCCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 369
QY 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
Db 370 AAAAATTTCAAGAGAACTCTGAAGATTTCTGTTTAAACAACCCCTTTGACTGCTGGGA 429

QY 421 CCAGCCCAAGATAA 435
Db 430 CCAGCCCAAGATAA 444

RESULT 3
US-09-322-409-121/C
; Sequence 121, Application US/09322409
; Patent No. 6471957
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/09/322,409
; EARLIER FILING DATE: 1999-05-28
; EARLIER FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus

Query Match 76.5%; Score 332.6; DB 3; Length 444;
Best Local Similarity 85.3%; Pred. No. 6.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGCATGCCGACCCACC 60
Db 435 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTGTTTACAGCATGCCGACCCACC 376
QY 61 CGCCAAACCAGCCCTGTCTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db 375 AGTTCAACCAGCTGTCTCACTCGGCCCTGGCAACAGCTGGATGCCATCAAGAGGCCCTG 316
QY 121 AGCCCTTCTGAACAACAGTAGTGACATGCTGTATCATGAATGAACAGTAGAGTCGTC 180
Db 315 AGCCCTTCTGAACAACAGTAGTGAAATACTGCTGTGATGAATGAACAGTAGAGTCGTC 256
QY 181 TCTGAAACGTTTGAAGCCGAGGAGTGACATGCCTGCAGACTCGCCTGAAGCTGTACAA 240
Db 255 TCTGAAATGTTTGAACCTTGAGGAGCGAAATGCCTGCAGACTCACCTAAAGCTGTACGAG 196
QY 241 CAGGCTTGGGGGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 195 CAGGCTTACGGGAGCCCTCATCAAGCTCAAGGAGCCCTCTGAGAATGATGCCAACCAT 136
QY 301 TACAAGCAGCACTGCCCCCACTTGGAAATCTCTGTGCAACCCAGATGATCACTTC 360
Db 135 TACAAGCAGCACTGCCCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 76
QY 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
Db 75 AAAAATTTCAAGAGAACTCTGAAGATTTCTGTTTAAACAACCCCTTTGACTGCTGGGA 16
QY 421 CCAGCCCAAGATAA 435
Db 15 CCAGCCCAAGATAA 1

RESULT 4
US-09-451-527-119
; Sequence 119, Application US/09451527
; Patent No. 6482403
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee

APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527
CURRENT FILING DATE: 1999-12-01
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119
LENGTH: 444
TYPE: DNA
ORGANISM: Felis catus
FEATURE:
NAME/KEY: CDS
LOCATION: (10)..(441)
US-09-451-527-119

Query Match 76.5%; Score 332.6; DB 3; Length 444;
Best Local Similarity 85.3%; Pred. No. 6.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCGCCACCCACC 60
DB 10 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCGCCACCCACC 69
QY 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB 70 AGTTCAACCCAGCTCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 129
QY 121 AGCTTCTTGAAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
DB 130 AGCTTCTTGAAACAACAGTAGTGAAATACTGCTGTGATGAATGAAGCAGTAGAAGTCGTC 189
QY 181 TCTGAAAGCTTTGACGCGGAGGAGCTGACATCGCTGCAGACTCGCTGAAGCTGTACAAA 240
DB 190 TCTGAAATGTTTGACCCCTGAGGAGCGGAATGCCCTGCAGACTCATTAAAGCTGTACGAG 249
QY 241 CAGGCTTTCGCGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
DB 250 CAGGCTTTCGCGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 309
QY 301 TACAAGCAGCACTGCCGCCACCCCTGGAACCTTCTGTGGAACCCAGATGATCACTTTC 360
DB 310 TACAAGCAGCACTGCCGCCCTTACTCCGGAACCCCTGTGGAACCCAGACTATCACTTTC 369
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
DB 370 AAAAATTTCAAGAAGAACTGAAGGATTTTCTGTTTAAACCCCTTTGACTGCTGGGA 429
QY 421 CCAGCCCAAGAGTAA 435
DB 430 CCAGACCAGAGTAA 444

RESULT 5
US-09-451-527-121/c
Sequence 121, Application US/09451527
Patent No. 6482403
GENERAL INFORMATION:
APPLICANT: Sim, Gek-kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/09/451,527

CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 09/322,409
EARLIER FILING DATE: 1999-05-28
EARLIER APPLICATION NUMBER: 60/087,306
EARLIER FILING DATE: 1998-05-29
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 121
LENGTH: 444
TYPE: DNA
ORGANISM: Felis catus
US-09-451-527-121

Query Match 76.5%; Score 332.6; DB 3; Length 444;
Best Local Similarity 85.3%; Pred. No. 6.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCGCCACCCACC 60
DB 435 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACCTGTTTACAGCATGCCGCCACCCACC 376
QY 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB 375 AGTTCAACCCAGCTCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 316
QY 121 AGCTTCTTGAAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
DB 315 AGCTTCTTGAAACAACAGTAGTGAAATACTGCTGTGATGAATGAAGCAGTAGAAGTCGTC 256
QY 181 TCTGAAAGCTTTGACGCGGAGGAGCTGACATGCCCTGCAGACTCGCTGAAGCTGTACAAA 240
DB 255 TCTGAAATGTTTGACCCCTGAGGAGCGGAATGCCCTGCAGACTCATTAAAGCTGTACGAG 196
QY 241 CAGGCTTTCGCGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
DB 195 CAGGCTTTCGCGGGCAGCCCTCATCAAGCTCGAAGGCCCTTGAGATGATGCCAGCCAT 136
QY 301 TACAAGCAGCACTGCCGCCACCCCTGGAACCTTCTGTGGAACCCAGATGATCACTTTC 360
DB 135 TACAAGCAGCACTGCCGCCCTTACTCCGGAACCCCTGTGGAACCCAGACTATCACTTTC 76
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG 420
DB 75 AAAAATTTCAAGAAGAACTGAAGGATTTTCTGTTTAAACCCCTTTGACTGCTGGGA 16
QY 421 CCAGCCCAAGAGTAA 435
DB 15 CCAGACCAGAGTAA 1

RESULT 6
US-10-262-439-119
Sequence 119, Application US/10262439
Patent No. 7026139
GENERAL INFORMATION:
APPLICANT: Sim, Gek-kee
APPLICANT: Yang, Shumin
APPLICANT: Dreitz, Matthew J.
APPLICANT: Wonderling, Ramani S.
TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: IM-2-C2
CURRENT APPLICATION NUMBER: US/10/262,439
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US/09/451,527
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 09/322,409
PRIOR FILING DATE: 1999-05-28
PRIOR APPLICATION NUMBER: 60/087,306
NUMBER OF SEQ ID NOS: 174
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 119

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; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)...(441)
US-10-262-439-119

Query Match      76.5%; Score 332.6; DB 5; Length 444;
Best Local Similarity 85.3%; Pred. No. 6.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGTGGTTTACAGATGCCCGCCACCCACC 60
   |||||
Db 10 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGTGGTTTACAGATCTCTGCACCCACC 69
   |||||

QY 61 CGCCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGAGCCCTG 120
   |||||
Db 70 AGTTCAACCAGCTCTGTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGAGCCCTG 129
   |||||

QY 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
   |||||
Db 130 AGCCTTCTGAACAAACAGTAGTGAATAAATGCTGTGATGAATGAAGCAGTAGAAGTCGTC 189
   |||||

QY 181 TCTGAAAGCTTTGACGCGGAGGAGCTGACATCGCTGCAAGTCTGCGCTGAAGCTGTACAAA 240
   |||||
Db 190 TCTGAAATGTTTGACCCCTGAGGAGCGGAATGCTGCGAGACTCACCTAAAGCTGTACGAG 249
   |||||

QY 241 CAGGGCTTGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
   |||||
Db 250 CAGGGCTTACGGGGAGGCTCATAGCCTCAAGGAGCCCTCTGAGATGATGCCAACCAT 309
   |||||

QY 301 TACAAGCAGCACTGCCCCCACCCTCGGAAACTTCTGTGCAACCCAGATATCACTTC 360
   |||||
Db 310 TACAAGCAGCACTGCCCCCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 369
   |||||

QY 361 AAAAGTTTCAAAAGAACTGAGGATTTCTGTTTGAGATCCCGTTGACTGCTGGGAAG 420
   |||||
Db 370 AAAAATTTCAAAGAGAATCTGAAGGATTTCTGTTTAAACCCCTTTGACTGCTGGGGA 429
   |||||

QY 421 CCAGCCCAAGATAA 435
   |||||
Db 430 CCAGACCAGAGATAA 444
   |||||

RESULT 7
US-10-262-439-121/c
; Sequence 121, Application US/10262439
; Patent No. 7026139
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; CURRENT FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus
US-10-262-439-121
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Query Match      76.5%; Score 332.6; DB 5; Length 444;
Best Local Similarity 85.3%; Pred. No. 6.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGTGGTTTACAGATGCCCGCCACCCACC 60
   |||||
Db 435 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGTGGTTTACAGATCTCTGCACCCACC 376
   |||||

QY 61 CGCCCAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGAGCCCTG 120
   |||||
Db 375 AGTTCAACCAGCTCTGTCACTCGGCCCTGGCAACACGTGGATGCCATCAAGAGAGCCCTG 316
   |||||

QY 121 AGCCTTCTGAACAAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
   |||||
Db 315 AGCCTTCTGAACAAACAGTAGTGAATAAATGCTGTGATGAATGAAGCAGTAGAAGTCGTC 256
   |||||

QY 181 TCTGAAAGCTTTGACGCGGAGGAGCTGACATCGCTGCGAGACTGCGCTGAAGCTGTACAAA 240
   |||||
Db 255 TCTGAAATGTTTGACCCCTGAGGAGCGGAATGCTGCGAGACTCACCTAAAGCTGTACGAG 196
   |||||

QY 241 CAGGGCTTGGGGGAGGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
   |||||
Db 195 CAGGGCTTACGGGGAGGCTCATCAGCCTCAAGGAGCCCTCTGAGAATGATGCCAACCAT 136
   |||||

QY 301 TACAAGCAGCACTGCCCCCACCCTCGGAAACTTCTGTGCAACCCAGATATCACTTC 360
   |||||
Db 135 TACAAGCAGCACTGCCCCCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACTTC 76
   |||||

QY 361 AAAAGTTTCAAAAGAACTGAGGATTTCTGTTTGAGATCCCGTTTGAAGTCTGGGAAG 420
   |||||
Db 75 AAAAATTTCAAAGAGAATCTGAAGGATTTCTGTTTAAACCCCTTTGACTGCTGGGGA 16
   |||||

QY 421 CCAGCCCAAGATAA 435
   |||||
Db 15 CCAGACCAGAGATAA 1
   |||||

RESULT 8
US-08-133-979A-10
; Sequence 10, Application US/08133979A
; Patent No. 5589582
; GENERAL INFORMATION:
; APPLICANT: Hawley, Robert J.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Rosa, Margaret D.
; APPLICANT: Monroy, Rodney L.
; APPLICANT: Schacter, Bernice Z.
; TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines Therei
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/133,979A
; FILING DATE: October 8, 1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Herron, Charles J.
; REGISTRATION NUMBER: 28,019
; REFERENCE/DOCKET NUMBER: 61750-79
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 10:
```


SEQUENCE CHARACTERISTICS:
LENGTH: 798 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-133-979A-10

Query Match 76.5%; Score 332.6; DB 2; Length 798;
Best Local Similarity 85.3%; Pred. No. 8.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACC 60
DB |||||
QY 30 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACC 89
DB |||||
QY 61 CGCCCAACCCAGCCCTGTCTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACCCTG 120
DB |||||
QY 90 CGCCCAACCCAGCCCTGTCTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACCCTG 149
DB |||||
QY 121 AGCCTTCTGAACCAACAGTAGTACACTGCTGCTATCATGAATGAACAGTAGAGTCGTC 180
DB |||||
QY 150 AGCCTTCTGAACCAACAGTAGTACACTGCTGCTATGAATGAACAGTAGAGTCGTC 209
DB |||||
QY 181 TCTGAAACCTTTGACGCCAGGAGGAGTGCATGCTGCAGACTCGGCTGAAGCTGTACAAA 240
DB |||||
QY 210 TGTGAATGTTTGAACCCAGGAGCGAGATGGTGCAGACTCGCTGAACCTGTACAA 269
DB |||||
QY 241 CAGGCTTGGCGGGCAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300
DB |||||
QY 270 CAGGCTTGGCGGGCAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 329
DB |||||
QY 301 TACAGCAGCACTGCCCCCAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 360
DB |||||
QY 330 TATGAGCAGCACTGCCCCCAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 389
DB |||||
QY 361 AAAAGTTTCAAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGAG 420
DB |||||
QY 390 AAAAGTTTCAAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGAG 449
DB |||||

RESULT 9

US-08-436-890-10
Sequence 10, Application US/08436890
Patent No. 5858963

GENERAL INFORMATION:

APPLICANT: Hawley, Robert J.
APPLICANT: Ponath, Paul D.
APPLICANT: Rosa, Margaret D.
APPLICANT: Monroy, Rodney L.
APPLICANT: Schacter, Bernice Z.

TITLE OF INVENTION:

Enhancement of Xenograft Tolerance and Porcine Cytokines There

NUMBER OF SEQUENCES:

24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA

ZIP:

07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.0
SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/436,890
FILING DATE: May 8, 1995

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Herron, Charles J.
REGISTRATION NUMBER: 28,019
REFERENCE/DOCKET NUMBER: 61750-139
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO:

10:

SEQUENCE CHARACTERISTICS:

LENGTH: 798 BASE PAIRS

TYPE: NUCLEIC ACID

STRANDEDNESS: DOUBLE

TOPOLOGY: LINEAR

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-08-436-890-10

Query Match 76.5%; Score 332.6; DB 2; Length 798;

Best Local Similarity 85.3%; Pred. No. 8.9e-88;

Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACC 60
DB |||||
QY 30 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACC 89
DB |||||
QY 61 CGCCCAACCCAGCCCTGTCTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACCCTG 120
DB |||||
QY 90 CGCCCAACCCAGCCCTGTCTCTGGGCACTGTGTTTACAGCATGCCGCCACCCACCCTG 149
DB |||||
QY 121 AGCCTTCTGAACCAACAGTAGTACACTGCTGCTATCATGAATGAACAGTAGAGTCGTC 180
DB |||||
QY 150 AGCCTTCTGAACCAACAGTAGTACACTGCTGCTATGAATGAACAGTAGAGTCGTC 209
DB |||||
QY 181 TCTGAAACCTTTGACGCCAGGAGGAGTGCATGCTGCAGACTCGGCTGAAGCTGTACAAA 240
DB |||||
QY 210 TGTGAATGTTTGAACCCAGGAGCGAGATGGTGCAGACTCGCTGAACCTGTACAA 269
DB |||||
QY 241 CAGGCTTGGCGGGCAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 300
DB |||||
QY 270 CAGGCTTGGCGGGCAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 329
DB |||||
QY 301 TACAGCAGCACTGCCCCCAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 360
DB |||||
QY 330 TATGAGCAGCACTGCCCCCAGCTCATCAAGCTCGAAGGCCCTTGAACCATGATGCCAGCCAC 389
DB |||||
QY 361 AAAAGTTTCAAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGAG 420
DB |||||
QY 390 AAAAGTTTCAAAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGAG 449
DB |||||

RESULT 10

US-08-451-213-10

Sequence 10, Application US/08451213

Patent No. 5863528

GENERAL INFORMATION:

APPLICANT: Hawley, Robert J.
APPLICANT: Ponath, Paul D.
APPLICANT: Rosa, Margaret D.
APPLICANT: Monroy, Rodney L.
APPLICANT: Schacter, Bernice Z.

TITLE OF INVENTION:

Enhancement of Xenograft Tolerance and Porcine Cytokines There

NUMBER OF SEQUENCES:

24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA

;; ZIP: 07068
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch diskette
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: MS-DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/451,213
;; FILING DATE: 26-MAY-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/133,979
;; FILING DATE: October 8, 1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Herron, Charles J.
;; REGISTRATION NUMBER: 28,019
;; REFERENCE/DOCKET NUMBER: 61750-79
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 798 BASE PAIRS
;; TYPE: NUCLEIC ACID
;; STRANDEDNESS: DOUBLE
;; TOPOLOGY: LINEAR
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-451-213-10

Query Match 76.5%; Score 332.6; DB 2; Length 798;
Best Local Similarity 85.3%; Pred. No. 8.9e-88;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 60
DB |||||
DB 30 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 89
QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB |||||
DB 90 CGCCCAACCCAGCCCTGTCTACCGGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 149
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180
DB |||||
DB 150 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 209
QY 181 TCTGAAACCTTTGAGCCCGCAGGAGCTGCATGCCTGCAGACTCGCCTGAACCTGTACAA 240
DB |||||
DB 210 TGTGAAATGTTTGACCCCGCAGGCGGACATGGGTGCAGACTCGCCTGAACCTGTACAA 269
QY 241 CAGGGCTTGGGGGCGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGTATGCCAGCCAC 300
DB |||||
DB 270 CAGGGCTTGGGGGCGAGCCTCATAGGCTCAAGAGGCCCTTGACTCTGTGTGCCAAGCAC 329
QY 301 TACAGCAGCACTGCCCGCCCGCCCTCGAACTTCTGTGCAACCCAGATGATCACTTC 360
DB |||||
DB 330 TATGAGCAGCACTGCCCGCCCGCCCTCGAAGAACTTCTGTGAAACCCAGTCTATCACTTC 389
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
DB |||||
DB 390 AAAAGTTTCAAGACAGTCTGAACAAATTTCTTTTACCATCCCTTTGACTGCTGGGG 449
QY 421 CCAGGCCAAGTAA 435
DB |||||
DB 450 CCAGTCAAAAAGTAA 464

RESULT 11
US-09-617-594A-9
; Sequence 9, Application US/09617594A
; Patent No. 6541458
; GENERAL INFORMATION:
; APPLICANT: Audonnet, et al.

;; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V
;; FILE REFERENCE: 454313-3151.1
;; CURRENT APPLICATION NUMBER: US/09/617,594A
;; CURRENT FILING DATE: 2000-07-14
;; PRIOR APPLICATION NUMBER: 60/193,332
;; PRIOR FILING DATE: 2000-03-30
;; PRIOR APPLICATION NUMBER: France 00 01761
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: France 99 09421
;; PRIOR FILING DATE: 1999-07-16
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 9
;; LENGTH: 432
;; TYPE: DNA
;; ORGANISM: Felis sp.
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(429)
;; OTHER INFORMATION: coding sequence of 3R4 feline GM-CSF gene
US-09-617-594A-9

Query Match 76.1%; Score 331.2; DB 3; Length 432;
Best Local Similarity 85.4%; Pred. No. 1.8e-87;
Matches 369; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 60
DB |||||
DB 1 ATGTGGCTGCAGAACCTGCTTCTCTGGGCACTGTGGTTTACAGCATGCCCGACCCACC 60
QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
DB |||||
DB 61 AGTTCACCCAGCTCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180
DB |||||
DB 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATGAATGAACAGTAGAGTCGTC 180
QY 181 TCTGAAACCTTTGAGCCCGCAGGAGCTGCATGCCTGCAGACTCGCCTGAAGCTGTACAA 240
DB |||||
DB 181 TCTGAAATGTTTGACCCCTGAGGAGCCGAAATGCTTGCAGACTCACCTAAAGCTGTACGAG 240
QY 241 CAGGGCTTGGGGGCGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGTATGCCAGCCAC 300
DB |||||
DB 241 CAGGGCTTACGGGCGAGCCTCATCAGCCTCAAGAGCCCTCTGAGGATGATGCCAACCAT 300
QY 301 TACAGCAGCACTGCCCGCCCGCCCTCGGAAACTTCTCTGTGCAACCCAGATGATCACTTC 360
DB |||||
DB 301 TACAGCAGCACTGCCCGCCCTTACTCCGGAAACCGCCCTGTGAAACCCAGACTATCACCTTC 360
QY 361 AAAAGTTTCAAAAAGAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAG 420
DB |||||
DB 361 AAAATTTCAAGAGAAATCTGAAGGATTTTCTGTTTAAATCCCTTTGACTGCTGGAAA 420
QY 421 CCAGCCCAAGAG 432
DB |||||
DB 421 CCAGTCAAGAG 432

RESULT 12
US-10-209-507-9
; Sequence 9, Application US/10209507
; Patent No. 6914134
; GENERAL INFORMATION:
; APPLICANT: Audonnet, et al.
; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V
; FILE REFERENCE: 454313-3151.2
; CURRENT APPLICATION NUMBER: US/10/209,507
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/617,594
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/193,332
; PRIOR FILING DATE: 2000-03-30

;; PRIOR APPLICATION NUMBER: France 00 01761
;; PRIOR FILING DATE: 2000-02-11
;; PRIOR APPLICATION NUMBER: France 99 09421
;; PRIOR FILING DATE: 1999-07-16
;; NUMBER OF SEQ ID NOS: 26
;; SOFTWARE: Patent in version 3.0
;; SEQ ID NO 9
;; LENGTH: 432
;; TYPE: DNA
;; ORGANISM: Felis sp.
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (1)..(429)
;; OTHER INFORMATION: coding sequence of 3R4 feline GM-CSF gene
US-10-209-507-9

Query Match 76.1%; Score 331.2; DB 3; Length 432;
Best Local Similarity 85.4%; Pred. No. 1.8e-87;
Matches 369; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAGAACTGCTTCTCTGGGCACCTGTGTTTACAGCATGCCCGCACCCACC 60
Db |||||
QY 1 ATGTGCTGCAGAACTGCTTCTCTGGGCACCTGTGTTTACAGCATGCCCGCACCCACC 60
Db |||||
QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
Db |||||
QY 61 AGTTCAACCCAGCTCTGTCACTCGGCCCTGGCAACACAGTGGATGCCATCAAGGAGGCCCTG 120
Db |||||
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
Db |||||
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
Db |||||
QY 181 TCTGAAAGCTTTGACGCGGAGGAGTGCATCGCTGCAGACTCGCTGAAGCTGTACAAA 240
Db |||||
QY 181 TCTGAAAGCTTTGACGCGGAGGAGTGCATCGCTGCAGACTCGCTGAAGCTGTACAAA 240
Db |||||
QY 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACATGCTGCTGGAG 420
Db |||||
QY 421 CCAGCCCAAG 432
Db |||||

RESULT 13
US-08-848-760B-8
; Sequence 8, Application US/08848760B
; Patent No. 6248721
; GENERAL INFORMATION:
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: Florida
; COUNTRY: United States of America
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/848,760B
;; FILING DATE: 25-Jan-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/838,701
;; FILING DATE: 09-APR-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: PACE, DORAN R.
;; REGISTRATION NUMBER: 38,261
;; REFERENCE/DOCKET NUMBER: CNG-i00C1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (352) 375-8100
;; TELEFAX: (352) 372-5800
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 435 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: other nucleic acid
;; DESCRIPTION: /desc = "DNA"
;; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-848-760B-8

Query Match 76.1%; Score 331; DB 3; Length 435;
Best Local Similarity 85.1%; Pred. No. 2e-87;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAGAACTGCTTCTCTGGGCACCTGTGTTTACAGCATGCCCGCACCCACC 60
Db |||||
QY 61 CGCCAAACCCAGCCCTGTCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG 120
Db |||||
QY 61 CGCTCGCCAGCCCGCAGCAGCGCCCTGGGAGCATGTGAATGCCATCAGGAGGCCCGG 120
Db |||||
QY 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
Db |||||
QY 121 CGTCTCTGAACTCAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180
Db |||||
QY 181 TCTGAAAGCTTTGACGCGGAGGAGTGCATCGCTGCAGACTCGCTGAAGCTGTACAAA 240
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QY 181 TCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCTGGAGCTGTACAAG 240
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QY 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTGGAAGGCCCTTGACATGATGCCAGCCAC 300
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QY 241 CAGGCTTTCGCGGGCAGCCTCATCAAGCTGGAAGGCCCTTGACATGATGCCAGCCAC 300
Db |||||
QY 301 TACAAGCAGCACTGCCCGCCCGCCCTCCAACTTCTGTGCAACCCAGATTATCACCTTT 360
Db |||||
QY 361 AAAAGTTTCAAAAAGAACCTGAAGATTTCGTGTTGAGATCCCGTTTGACTGCTGGAG 420
Db |||||
QY 361 GAAAGTTTCAAAAAGAACCTGAAGATTTCGTGTTGAGATCCCGTTTGACTGCTGGAG 420
Db |||||
QY 421 CCAGCCCAAGTAA 435
Db |||||

RESULT 14
US-09-826-025-8
; Sequence 8, Application US/09826025
; Patent No. 6730512
; GENERAL INFORMATION:
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Combination Immunogene Therapy
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200

```

, CITY: San Francisco
, STATE: California
, COUNTRY: United States of America
, ZIP: 94104
,
, COMPUTER READABLE FORM:
,
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: Patent In Release #1.0.
,
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/826,025
, FILING DATE: 04-Apr-2001
, CLASSIFICATION: <unknown>
,
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 08/838,702
, FILING DATE: <unknown>
, ATTORNEY/AGENT INFORMATION:
, NAME: Ingolia, Diane E.
, REGISTRATION NUMBER: 40,027
, REFERENCE/DOCKET NUMBER: CHANG-02
,
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (415) 705-8410
, TELEFAX: (415) 397-8338
,
, INFORMATION FOR SEQ ID NO: 8:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 435 base pairs
, TYPE: nucleic acid
, STRANDEDNESS: double
, TOPOLOGY: linear
,
, MOLECULE TYPE: other nucleic acid
, DESCRIPTION: /desc = "DNA"
, SEQUENCE DESCRIPTION: SEQ ID NO: 8:
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, US-09-826-025-8

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Query Match	76.1%	Score 331;	DB 3;	Length 435;
Best Local Similarity	85.1%	Pred. No. 2e-87;		
Matches 370;	Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;
QY	1	ATGTGGCTGCAGAAACCTGCTTCTTCTGGGCACCTGTGGTTTACAGCATGCCGCCACCCACC	60	
DB	1	ATGTGGCTGCAGAGCCGTGCTCTTGGGCACCTGTGGCCTGCAGCATCTCTGCACCCGCC	60	
QY	61	CGCCAAACCCAGCCCTGTCTATCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120	
DB	61	CGCTCGCCACGCCCCAGCAGCCGACCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGG	120	
QY	121	AGCCCTTCTGAAACACAGTAGTGCACCTGCTGCTTATCATGAATGAAACAGTAGAAGTCGTC	180	
DB	121	CGTCTCCTGNAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAATCATC	180	
QY	181	TTCTGAAACGTTTGACGCCGAGGAGCTGACATGCGCTGCAGACTGCGCTGAAGCTGTACAA	240	
DB	181	TCAGAAATGTTTGACCTTCCAGGAGCCGACCTGCGCTACAGACCCGCTGGAGCTGTACAAG	240	
QY	241	CAGGGCTTGGGGGCGAGCCCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCAC	300	
DB	241	CAGGGCTTGGGGGCGAGCCCTTACCAAGCTCAAGGCCCTTGACCATGATGGCCAGCCAC	300	
QY	301	TACAAGCAGCACTGCCGCCCCACCTCGTGGAACCTTCGTGTGCAACCCAGATGATCACTTC	360	
DB	301	TACAAGCAGCACTGCCCTCCAAACCCCGGAACCTTCCTGTGTGCAACCCAGATGATCACCTTT	360	
QY	361	AAAAGTTTCAAAAGACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG	420	
DB	361	GAAAGTTTCAAGAGAACCTGAAGGACTTCTGCTTGTCACTCCCTTTGACTGCTGGAG	420	
QY	421	CCAGCCCGAAGTAA	435	
DB	421	CCAGTCCAGAGTGA	435	

RESULT 15

• US-09-543-679A-2706

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: Sequence 2706, Application US/09543679A
: Patent No. 7034007
: GENERAL INFORMATION:
: APPLICANT: NYCE, Jonathan W.
: TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
: COMPOSITIONS, KIT & METHOD FOR TREATMENT
: OF AIRWAY DISORDERS ASSOCIATED WITH
: BRONCHOCONSTRICTION, LUNG INFLAMMATION,
:
: NUMBER OF SEQUENCES: 3111
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
: STREET: 7 Clarke Drive
: CITY: Cranbury
: STATE: NJ
: COUNTRY: USA
: ZIP: 08512
: COMPUTER READABLE FORM:
: MEDIUM TYPE: CD-R
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: N/A
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/543,679A
: FILING DATE: 13-Apr-2000
: CLASSIFICATION: UNKNOWN
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/127,958
: FILING DATE: 1998-08-03
: ATTORNEY/AGENT INFORMATION:
: NAME: Amzel, Viviana
: REGISTRATION NUMBER: 30,930
: REFERENCE/DOCKET NUMBER: EPI-0067191b
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 609-409-3035
: TELEFAX: 413-254-9245
: TELEX: <Unknown>
:
: INFORMATION FOR SEQ ID NO: 2706:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 789 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 2706
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: US-09-543-679A-2706

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Query Match	76.1%	Score 331	DB 5	Length 789
Best Local Similarity	85.1%	Pred. No. 2.6e-87		
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Db	33	ATGTGGCTGCAGAGCCTGCTCTTGGGCACATGTGGCCTGCAGCATCTCTGCACCCGCC	92	
Qy	61	CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120	
Db	93	CGTCCGCCAGCCCCAGCAGCAGCCTGGAGCATGTGAATGCCATCCAGGAGCCCGG	152	
Qy	121	AGCCTTCTGAACAAACAGTAGTAGACATGCTGCTATCATGAATGAAACAGTAGAAGTCGT	180	
Db	153	CGTCTCTGAACCTGTAGTAGAGACATGCTGCTGAGATGAATGAAACAGTAGAAGTCATC	212	
Qy	181	TCTGAACGTTTGACGCCGAGGAGCTGACATGCTGCAGACTGCCCTGAAGCTGTACAAA	240	
Db	213	TCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCCTACAGACCCGCTGGAGCTGTACAG	272	
Qy	241	CAGGCTTTCGGGGCAGCCTCATCAAGCTCGAAGGCCCTTGCACCATGATGGCCAGCCAC	300	
Db	273	CAGGCCCTCGGGGAGCCTCACCAAGCTCAAGSGCCCTTGCACCATGATGGCCAGCCAC	332	
Qy	301	TACAAGCAGCACTGCCCCCCCGACCTTGGAAAATTCTGTGCAACCCAGATGATCACCTTC	360	
Db	333	TACAAGCAGCACTGCCCTTCAACCCCGGAACTTCTGTGCAACCCAGATGATCACCTTT	392	

Qy	361	AAAAGTTTCAAAAGAACCTGAAGGATTTCTGTGTTTGAGATCCCGTTTGACTGCTGGAAG	420
Db	393	GAAAGTTTCAAAAGAGAACCTGAAGGACTTCTGTGCTTGTCAATCCCTTTGACTGCTGGGAG	452
Qy	421	CCAGCCCAGAGTAA	435
Db	453	CCAGTCCAGGAGTGA	467

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OM nucleic - nucleic search, using sw model

Run on: May 26, 2006, 01:24:10 ; Search time 1032 Seconds
(without alignments)
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Title: US-10-614-481-8
Perfect score: 435
Sequence: 1 atgtggctgcagaaactgct.....ggaagccagccagagtaa 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18992170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
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- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	10	US-10-614-481-8
2	332.6	76.5	444	6	Sequence 8, Appli
3	332.6	76.5	444	6	Sequence 119, App
4	332.6	76.5	444	7	US-10-218-654-119
5	332.6	76.5	444	7	US-10-262-439-119
6	331.2	76.1	432	6	US-10-262-439-121
7	331	76.1	435	3	US-10-209-507-9
8	331	76.1	435	3	US-09-826-025-8
9	331	76.1	435	6	US-10-083-590-14
10	331	76.1	435	8	US-10-411-037-17
11	331	76.1	435	8	US-10-411-026-17
12	331	76.1	435	8	US-10-410-962-17
13	331	76.1	435	8	US-10-411-049-17
14	331	76.1	435	8	US-10-410-930-17
15	331	76.1	435	8	US-10-410-997-17
16	331	76.1	435	8	US-10-411-012-17
17	331	76.1	435	8	US-10-287-994-17
17	331	76.1	435	8	US-10-410-913-17

18	331	76.1	435	9	US-10-785-377-8	Sequence 8, Appli
19	331	76.1	435	9	US-10-410-380-17	Sequence 17, Appl
20	331	76.1	435	10	US-10-410-897-17	Sequence 17, Appl
21	331	76.1	435	10	US-10-492-261-17	Sequence 17, Appl
22	331	76.1	435	11	US-10-937-658-2	Sequence 2, Appli
23	331	76.1	435	11	US-10-183-205-17	Sequence 17, Appl
24	331	76.1	435	16	US-11-201-384-16	Sequence 16, Appl
25	331	76.1	448	8	US-10-609-346-19	Sequence 19, Appl
26	331	76.1	781	8	US-10-447-315-20	Sequence 20, Appl
27	331	76.1	789	7	US-10-131-985-16	Sequence 16, Appl
28	331	76.1	789	9	US-10-901-417-16	Sequence 16, Appl
29	331	76.1	900	10	US-10-925-205-10	Sequence 10, Appl
30	331	76.1	900	15	US-11-066-480-10	Sequence 10, Appl
31	331	76.1	1172	10	US-10-925-205-5	Sequence 5, Appli
32	331	76.1	1172	15	US-11-066-480-5	Sequence 5, Appli
33	329.6	75.8	432	6	US-10-218-654-122	Sequence 122, App
34	329.6	75.8	432	6	US-10-218-654-123	Sequence 123, App
35	329.6	75.8	432	6	US-10-209-507-7	Sequence 7, Appli
36	329.6	75.8	432	7	US-10-262-439-122	Sequence 123, App
37	329.6	75.8	432	7	US-10-262-439-123	Sequence 123, App
38	329.6	75.8	1833	3	US-09-783-708-2	Sequence 2, Appli
39	329.4	75.7	435	7	US-10-188-056-32	Sequence 32, Appli
40	329.4	75.7	435	10	US-10-775-204-15	Sequence 15, Appl
41	329.4	75.7	435	10	US-10-775-204-16	Sequence 16, Appl
42	329.4	75.7	435	10	US-10-775-204-108	Sequence 108, App
43	329.4	75.7	435	10	US-10-775-204-109	Sequence 109, App
44	329.4	75.7	496	7	US-10-267-384-191	Sequence 191, App
45	329.4	75.7	505	9	US-10-688-845-82	Sequence 82, Appl

ALIGNMENTS

RESULT 1

US-10-614-481-8
; Sequence 8, Application US/10614481
; Publication No. US20050059121A1
; GENERAL INFORMATION:
; APPLICANT: Bublout, et al.
; TITLE OF INVENTION: Equine GM-CSF
; FILE REFERENCE: 454313-2334.1
; CURRENT APPLICATION NUMBER: US/10/614,481
; PRIOR FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/589,460
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/138,843
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Equine sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(432)
; OTHER INFORMATION: coding sequence of equine GM-CSF gene
US-10-614-481-8

Query Match 100.0%; Score 435; DB 10; Length 435;
Best Local Similarity 100.0%; Pred. No. 8.7e-131;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGTGGCTGCAGAACTGCTCTTCTTGGGCACTGGTTTACAGCATGCCGCCACC	60
DB	1	ATGTGGCTGCAGAACTGCTCTTCTTGGGCACTGGTTTACAGCATGCCGCCACC	60
QY	61	CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG	120
DB	61	CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGCCCTG	120
QY	121	AGCCTTCTTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC	180
DB	121	AGCCTTCTTGAAACACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC	180

Db 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAATGAACAGTAGAGTCGTC 180
Qy 181 TCTGAAACGTTTGGCGCGAGAGCTGACATGCTCTGCAGACTCGCTGAAAGCTGTACAAA 240
Db 181 TCTGAAACGTTTGGCGCGAGAGCTGACATGCTCTGCAGACTCGCTGAAAGCTGTACAAA 240
Qy 241 CAGGCTTGGCGGAGAGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGCTTGGCGGAGAGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Qy 301 TACAGCAGCAGCTGCCCCCACCCTCGAAACTTCTGTGCAACCCAGATGATCACCTTC 360
Db 301 TACAGCAGCAGCTGCCCCCACCCTCGAAACTTCTGTGCAACCCAGATGATCACCTTC 360
Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGAATGCTGGAAG 420
Db 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGAATGCTGGAAG 420
Qy 421 CCAGCCCAAGTAA 435
Db 421 CCAGCCCAAGTAA 435

RESULT 2

US-10-218-654-119
; Sequence 119, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)...(441)
US-10-218-654-119

Query Match 76.5%; Score 332.6; DB 6; Length 444;
Best Local Similarity 85.3%; Pred. No. 2,1e-97;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60
Db 10 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 69
Qy 61 CGCCAAACCCAGCCTGCTCACTCGGCCCTGGCAGATGTGGATGCCATCAAGGAGGCCCTG 120
Db 70 AGTTCAACCCAGCCTGCTCACTCGGCCCTGGCAGATGTGGATGCCATCAAGGAGGCCCTG 129
Qy 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180
Db 130 AGCCTTCTGAACAACAGTAGTAGTAATACTGTGTGATGAATGAAGCAGTAGAGTCGTC 189
Qy 181 TCTGAAACGTTTGGCGCGAGAGCTGACATGCCCTGCAGACTCGCTGAAAGCTGTACAAA 240
Db 190 TCTGAAATGTTTGAACCTTGAGGAGCGAAATGCTCTGCAGACTCACCTAAAGCTGTACGAG 249
Qy 241 CAGGCTTGGCGGAGAGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300

Db 250 CAGGCTTACGGGAGAGCTCATCAGCTCAAGAGCCTCTGAGATGATGCGCAACCAT 309
Qy 301 TACAAGCAGCAGCTGCCCCCACCCTGGAATCTCTGTGCAACCCAGATGATCACCTTC 360
Db 310 TACAAGCAGCAGCTGCCCCCTTACTCCGAAACGCCCTGTGAAACCCAGACTATCACCTTC 369
Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGAATGCTGGAAG 420
Db 370 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTAAACAACCCCTTTGACTGCTGGGA 429
Qy 421 CCAGCCCAAGTAA 435
Db 430 CCAGCCCAAGTAA 444

RESULT 3

US-10-218-654-121/c
; Sequence 121, Application US/10218654
; Publication No. US20030099609A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Kee
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES, AND USES THEREOF
; FILE REFERENCE: IM-2-C1
; CURRENT APPLICATION NUMBER: US/10/218,654
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus
US-10-218-654-121

Query Match 76.5%; Score 332.6; DB 6; Length 444;
Best Local Similarity 85.3%; Pred. No. 2,1e-97;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
Qy 1 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60
Db 435 ATGTGGCTGCAGAACTGCTTCTCTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 376
Qy 61 CGCCAAACCCAGCCTGCTCACTCGGCCCTGGCAGATGTGGATGCCATCAAGGAGGCCCTG 120
Db 375 AGTTCAACCCAGCCTGCTCACTCGGCCCTGGCAGATGTGGATGCCATCAAGGAGGCCCTG 316
Qy 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAGTCGTC 180
Db 315 AGCCTTCTGAACAACAGTAGTAGTAATACTGTGTGATGAATGAAGCAGTAGAGTCGTC 256
Qy 181 TCTGAAACGTTTGGCGCGAGAGCTGACATGCCCTGCAGACTCGCTGAAAGCTGTACAAA 240
Db 255 TCTGAAATGTTTGAACCTTGAGGAGCGAAATGCTCTGCAGACTCACCTAAAGCTGTACGAG 196
Qy 241 CAGGCTTGGCGGAGAGCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 195 CAGGCTTACGGGAGAGCTCATCAAGCTCGAAGGCCCTTGAGATGATGCCAACCAT 136
Qy 301 TACAAGCAGCAGCTGCCCCCACCCTCGAAACTTCTGTGCAACCCAGATGATCACCTTC 360
Db 135 TACAAGCAGCAGCTGCCCCCTTACTCCGAAACGCCCTGTGAAACCCAGACTATCACCTTC 76
Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTGAGATCCCGTTTGAATGCTGGAAG 420
Db 75 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTTTAAACAACCCCTTTGACTGCTGGGA 16

QY 421 CCAGCCCAAGTAA 435
Db 15 CCAGACCAGTAA 1

RESULT 4
US-10-262-439-119
; Sequence 119, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus
; NAME/KEY: CDS
; LOCATION: (10)..(441)
US-10-262-439-119

Query Match 76.5%; Score 332.6; DB 7; Length 444;
Best Local Similarity 85.3%; Pred. No. 2.1e-97;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGACCCACC 60
Db 10 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGACCCACC 69

QY 61 CCGCAACCCAGCCCTGCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db 70 AGTTCAACCAGCTCTGTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 129

QY 121 AGCCTTCTGAACAACAGTAGTGACACTGTCTATCATGAATGAACAGTAGAAGTCGTC 180
Db 130 AGCCTTCTGAACAACAGTAGTGAAATACTGTGTGATGAATGAAGCACTAGAGTCGTC 189

QY 181 TCTGAAACCTTTGACCCGAGGAGTGACATGCTGCGACACTCGCTGAAGCTGTACAA 240
Db 190 TCTGAAATGTTTGACCCCTGAGGAGCGAAATGCTGCGACACTCACCTAAAGCTGTACGAG 249

QY 241 CAGGCTTCGCGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 250 CAGGCTTCGCGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 309

QY 301 TACAAGCAGCACTGCCCCCTTACTCTGTGCAACCCAGATGATCACTTTC 360
Db 310 TACAAGCAGCACTGCCCCCTTACTCTGTGCAACCCAGATGATCACTTTC 369

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTCTGTTGAGATCCCGTTTCACTGCTGGAAG 420
Db 370 AAAAATTTCAAAAGAGAACTGAAGGATTTCTGTTTAAACACCCCTTTGACTGCTGGGA 429

QY 421 CCAGCCCAAGTAA 435
Db 430 CCAGACCAGTAA 444

RESULT 5
US-10-262-439-121/c
; Sequence 121, Application US/10262439
; Publication No. US20030143196A1
; GENERAL INFORMATION:
; APPLICANT: Sim, Gek-Ke
; APPLICANT: Yang, Shumin
; APPLICANT: Dreitz, Matthew J.
; APPLICANT: Wonderling, Ramani S.
; TITLE OF INVENTION: CANINE AND FELINE IMMUNOREGULATORY PROTEINS, NUCLEIC
; FILE REFERENCE: IM-2-C2
; CURRENT APPLICATION NUMBER: US/10/262,439
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: US/09/451,527
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: 09/322,409
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/087,306
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 121
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Felis catus
US-10-262-439-121

Query Match 76.5%; Score 332.6; DB 7; Length 444;
Best Local Similarity 85.3%; Pred. No. 2.1e-97;
Matches 371; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGACCCACC 60
Db 435 ATGTGGCTGCAGAACCTGCTTCTTCTGGGCACTGTGTTTACAGCATGCCGACCCACC 376

QY 61 CCGCAACCCAGCCCTGCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db 375 AGTTCAACCAGCTCTGTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 316

QY 121 AGCCTTCTGAACAACAGTAGTGACACTGTCTATCATGAATGAACAGTAGAAGTCGTC 180
Db 315 AGCCTTCTGAACAACAGTAGTGAAATACTGTGTGATGAATGAAGCACTAGAAGTCGTC 256

QY 181 TCTGAAACCTTTGACCCGAGGAGTGACATGCTGCGACACTCGCTGAAGCTGTACAA 240
Db 255 TCTGAAATGTTTGACCCCTGAGGAGCGAAATGCTGCGACACTCACCTAAAGCTGTACGAG 196

QY 241 CAGGCTTCGCGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 195 CAGGCTTCGCGGGGAGCCTCATCAAGCTCGAAGGCCCTTGAGATGATGCCAGCCAT 136

QY 301 TACAAGCAGCACTGCCCCCTTACTCTGTGCAACCCAGATGATCACTTTC 360
Db 135 TACAAGCAGCACTGCCCCCTTACTCTCGGAAACCCCTGTGAAACCCAGACTATCACCTTC 76

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTCTGTTGAGATCCCGTTTCACTGCTGGAAG 420
Db 75 AAAAATTTCAAAAGAGAACTGAAGGATTTCTGTTTAAACACCCCTTTGACTGCTGGGA 16

QY 421 CCAGCCCAAGTAA 435
Db 15 CCAGACCAGTAA 1

RESULT 6
US-10-209-507-9
; Sequence 9, Application US/10209507
; Publication No. US20030109033A1
; GENERAL INFORMATION:
; APPLICANT: Audonnet, et al.
; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V

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; FILE REFERENCE: 454313-3151.2
; CURRENT APPLICATION NUMBER: US/10/209,507
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/617,594
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/193,332
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: France 00 01761
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: France 99 09421
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Felis sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(429)
; OTHER INFORMATION: coding sequence of 3R4 feline GM-CSF gene
US-10-209-507-9

Query Match      76.1%; Score 331.2; DB 6; Length 432;
Best Local Similarity 85.4%; Pred. No. 6e-97;
Matches 369; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGGTTTACAGATGCCGCCACCCACC 60
Db 1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGGTTTACAGATGCCGCCACCCACC 60

QY 61 CGCCAAACCCAGCCCTGCTACTCGGCCCTGGGAGCATGGATGCCATCAAGAGGCCCTG 120
Db 61 AGTTCAACCCAGCTGCTCACTCGGCCCTGGCAACAGCTGGATGCCATCAAGAGGCCCTG 120

QY 121 AGCCTTCTGAAACAACAGTAGTGACACTGCTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 AGCCTTCTGAAACAACAGTAGTGAAATACTGCTGTGATGAATGAAGAGTAGAAGTCGTC 180

QY 181 TCTGAAACGTTTGACCGCCGAGGAGCTGACATGCTGCTATCATGAATGAACAGTAGAAGTCGTC 240
Db 181 TCTGAAATGTTTGACCTTGAGGAGCGGAAATGCTCTGCGAGACTCACCTAAAGCTGTACGAG 240

QY 241 CAGGCTTTCGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGCTTTCGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGAGGATGATGCCCAACCAT 300

QY 301 TACAAGCAGACTGCGCCGCCACCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC 360
Db 301 TACAAGCAGACTGCGCCCTTACTCGGAAACGCCCTGTGAAACCCAGACTATCACCTTC 360

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAG 420
Db 361 AAAAATTTCAAGAGAACTGAAGGATTTCTGTGTTTAAACATCCCTTTGACTGTGGAA 420

QY 421 CCAGCCCAAGAG 432
Db 421 CCAGTCAAGAG 432
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RESULT 7

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US-09-826-025-8
; Sequence 8, Application US/09826025
; Patent No. US20020162123A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Combination Immunogene Therapy
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
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RESULT 8

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US-10-083-590-14
; Sequence 14, Application US/10083590
; Publication No. US20030027257A1
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; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/826,025
; FILING DATE: 04-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/838,702
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ingolia, Diane E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: CHANG-02687
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-826-025-8
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Query Match 76.1%; Score 331; DB 3; Length 435;

Best Local Similarity 85.1%; Pred. No. 7e-97;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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QY 1 ATGTGGCTGCAGAACTGCTTCTTCTGGGCACTGGTTTACAGCATGCCGCCACCCACC 60
Db 1 ATGTGGCTGCAGAGCTGCTGCTCTTGGGCACTGGGCTGCAGCATCTCTGCACCCGCC 60

QY 61 CGCCAAACCCAGCCCTGCTCACTCGGCCCTGGGAGCATGGATGCCATCAAGAGGCCCTG 120
Db 61 CGCTCGCCAGCCCGCAGCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120

QY 121 AGCCTTCTGAAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 CGTCTCTCTGAAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATC 180

QY 181 TCTGAAACGTTTGACCGCGAGGAGCTGACATGCTGCGAGACTCGGCTGGAAGCTGTACAAA 240
Db 181 TCAGAAATGTTTGACCTCCAGGAGCCGACCTGCTTACAGACCCGCTGGAGCTGTACAG 240

QY 241 CAGGCTTTCGGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGSCCTTCGGGGGAGCCTCACCAAGCTCAAGGCCCTTCAAGGCCTTGCACCATGATGCCAGCCAC 300

QY 301 TACAAGCAGACTGCGCCGCCACCTTGGAAACTTCTGTGTCGAAACCCAGATGATCACCTTC 360
Db 301 TACAAGCAGACTGCGCTCCAAACCCCGGAAACTTCTCTGTGCAACCCAGATTTATCACCTTT 360

QY 361 AAAAGTTTCAAAAGAACCTGAAGGATTTCTGTGTTGAGATCCCGTTTGACTGTGGAG 420
Db 361 GAAAGTTTCAAAAGAGAACTGAGGACTTTCTGTGTTGTCATCCCTTTGACTGTCTGGGAG 420

QY 421 CCAGCCCAAGAGTAA 435
Db 421 CCAGTCCAGGAGTGA 435
```



```
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-026-17
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Query Match 76.1%; Score 331; DB 8; Length 435;
Best Local Similarity 85.1%; Pred. No. 7e-97;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
Db 1 ATGTGCTGCAGAGCCTGCTCTTGGGCACTGTGGGCTGCGAGCATCTCTGCACCCGCC 60

QY 61 CGCCAAACCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db 61 CGCTCGCCAGCCCGCCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120

QY 121 AGCCTTCTGAACAAAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 CGTCTCTGAACTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATC 180

QY 181 TGTGAACCTTTGACGCCGAGAGTGACATGCTCTGAGAGTGAAGTGTACAAA 240
Db 181 TCAGAAATGTTGAACTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATC 180

QY 241 CAGGGCTTCGGGGGAGCGCTCATCAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGGCTTCGGGGGAGCGCTCACAAAGCTCAAGGGGCCCTTGACCATGATGCCAGCCAC 300

QY 301 TACAAGCAGACTGCCCCCACCCTGGAAACTTCTGTGCAACCCAGATGATCACTTTC 360
Db 301 TACAAGCAGACTGCCCCCACCCTGGAAACTTCTGTGCAACCCAGATGATCACTTTC 360

QY 361 AAAAGTTTCAAAAGAACTGAAGAGATTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG 420
Db 361 GAAAGTTTCAAAAGAACTGAAGAGATTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG 420

QY 421 CCAGCCCAAGAGTAA 435
Db 421 CCAGTCCAGGAGTGA 435
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RESULT 11
US-10-410-962-17
; Sequence 17, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Niose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
```

```
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Caryn
; TITLE OF INVENTION: GLYCOCONJUGATE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-962-17
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Query Match 76.1%; Score 331; DB 8; Length 435;
Best Local Similarity 85.1%; Pred. No. 7e-97;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 1 ATGTGCTGCAGAACCTGCTTCTTCTGGGCACTGTGGTTTACAGCATGCCGCCACCCACC 60
Db 1 ATGTGCTGCAGAGCCTGCTCTTGGGCACTGTGGGCTGCGAGCATCTCTGCACCCGCC 60

QY 61 CGCCAAACCAGCCCTGCTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db 61 CGCTCGCCAGCCCGCCAGCAGCCCTGGGAGCATGTGAATGCCATCCAGAGGCCCGG 120

QY 121 AGCCTTCTGAACAAAGTAGTGACACTGCTCTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 CGTCTCTGAACTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATC 180

QY 181 TGTGAACCTTTGACGCCGAGAGTGACATGCTCTGAGAGTGAAGTGTACAAA 240
Db 181 TCAGAAATGTTGAACTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATC 180

QY 241 CAGGGCTTCGGGGGAGCGCTCATCAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGGCTTCGGGGGAGCGCTCACAAAGCTCAAGGGGCCCTTGACCATGATGCCAGCCAC 300

QY 301 TACAAGCAGACTGCCCCCACCCTGGAAACTTCTGTGCAACCCAGATGATCACTTTC 360
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QY 361 AAAAGTTTCAAAAGAACTGAAGAGATTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG 420
Db 361 GAAAGTTTCAAAAGAACTGAAGAGATTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG 420

QY 421 CCAGCCCAAGAGTAA 435
Db 421 CCAGTCCAGGAGTGA 435
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RESULT 12
US-10-411-049-17
; Sequence 17, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
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/ APPLICANT: Neose Technologies, Inc.
/ APPLICANT: Defrees, Shawn
/ APPLICANT: Zopt, David
/ APPLICANT: Bayer, Robert
/ APPLICANT: Hakes, David
/ APPLICANT: Chen, Xi
/ APPLICANT: Bowe, Caryn
/ TITLE OF INVENTION: INTERFERON ALPHA
/ TITLE OF INVENTION: ALPHA
/ FILE REFERENCE: 040853-01-5055
/ CURRENT APPLICATION NUMBER: US/10/4/04-09
/ CURRENT FILING DATE: 2003-04-09
/ PRIOR APPLICATION NUMBER: US 60/328
/ PRIOR FILING DATE: 2001-10-10
/ PRIOR APPLICATION NUMBER: US 60/344
/ PRIOR FILING DATE: 2001-10-19
/ PRIOR APPLICATION NUMBER: US 60/387
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: US 60/391
/ PRIOR FILING DATE: 2002-06-25
/ PRIOR APPLICATION NUMBER: US 60/396
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: US 60/404
/ PRIOR FILING DATE: 2002-08-16
/ PRIOR APPLICATION NUMBER: US 60/407
/ PRIOR FILING DATE: 2002-08-28
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 17
/ LENGTH: 435
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-411-049-17

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Query Match	76.1%;	Score 331;	DB 8;	Length 435;
Best Local Similarity	85.1%;	Pred. No. 7e-97;		
Matches 370;	Conservative 0;	Mismatches 65;	Indels 0;	Gaps 0;

QY	1	ATGTGGCTGCAGAACCTGCTCTCTCTGGGCACCTGTGTTTTACAGCATGCCGCCGACCCACC	60
DB	1	ATGTGGCTGCAGAGCCTGCTCTTGTGGCACCTGTGGCCTTGCAGCATCTCTGCACCCGCC	60
QY	61	CGCCAAACCCAGCCCTGTCACTCGGCCCTGGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120
DB	61	CGTCGCCCCAGCCCCCAGCAGCCTGGAGCATGTGAATGCCATCCAGAGGCCCGG	120
QY	121	AGCCTCTGAACAAACAGTAGTGACACTGCTGCTATCATGAATGAAACAGTAGAAGTCGT	180
DB	121	CGTCTCTGAAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATC	180
QY	181	TCTGAAACGTTTGACGCCGAGGAGCTGACATGCTCTGCAGACTCGCCTGGAAGCTGTACAA	240
DB	181	TCAGAAATGTTTGACCTCCAGGAGCCGACCTGCTGCCTACAGACCCGCCCTGGAGCTGTACA	240
QY	241	CAGGGCTTCGGGGCAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGGCCAGCCAC	300
DB	241	CAGGGCTTCGGGGCAGCCTCACCAAGCTCAAGGCCCTTGACCATGATGGCCAGCCAC	300
QY	301	TACAAGCAGCACTGCCCCCCCCCCTCGAAACTTCCTGTGTGCAACCCAGATGATCACCTTC	360
DB	301	TACAAGCAGCACTGCCCCCTCAACCCCGAAACTTCCTGTGTGCAACCCAGATGATCACCTTT	360
QY	361	AAAAGTTTCAAAAGAAACCTGAAGGATTTTCTGTTTGAGATCCCGTTTGACTGCTGGAAG	420
DB	361	GAAAGTTTCAAGAGAACCTGAAGGACTTCTGCTGCTCATCCCCCTTGACTGCTGGAG	420
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DB	421	CCAGTCCAGAGTGA	435

RESULT 13
US-10-410-930-17

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; Sequence 17, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayfer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5056
; CURRENT APPLICATION NUMBER: US/10/410,930
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-410-930-17

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Query Match	76.1%	Score 331;	DB 8;	Length 435;
Best Local Similarity	85.1%	Pred. No. 7e-97;		
Matches	370;	Conservative	0;	Mismatches 65; Indels 0; Gaps 0;
Qy	1	ATGTGGCTGCAGAACCTGCTCTTCTTGGGCACTGTGTGTTTACAGCATGCCCGCACCCACC	60	
Db	1	ATGTGGCTGCAGAGCCCTGCTCTTGGGCACTGTGGCCCTGCAGCATCTCTGCACCCGCC	60	
Qy	61	CGCCAAACCCAGCCCTGTCTACTCGGCCCTGCAGCATGTGGATGCCATCAAGGAGGCCCTG	120	
Db	61	CGTCCGCCAGCCCCAGCAGCGACCCCTGGAGCATGTGAATGCCATCCAGGAGGCCCG	120	
Qy	121	AGCCTTCTGAACAACAGTAGTGACACTGCTGCTATCATGAATGAACAGTAGAAGTCGTC	180	
Db	121	CGTCTCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAACAGTAGAAGTCATC	180	
Qy	181	TCTGAACGTTTGAGCGCCGAGGAGCTGACATGCCCTGCAGACTCGCCCTGAAGCTGTACAA	240	
Db	181	TCAGAAATGTTTGACCTTCCAGGAGCCGACCTGCCCTACAGACCCGCTGGAGCTGTACAAG	240	
Qy	241	CAGGGCTTCGGGGGAGCCTCATCAGCTCGAAGGCCCTTGACCATGATGGCCAGCCAC	300	
Db	241	CAGGGCTTCGGGGGAGCCTCACAAAGCTCAAGGGCCCTTGACCATGATGGCCAGCCAC	300	
Qy	301	TACAAGCAGCACTGCCCCCCACCTCTGGAACCTTCTGTGCAACCCAGATGATCACCTTC	360	
Db	301	TACAAGCAGCACTGCCCTCCAAACCCGGAACCTTCTGTGCAACCCAGATGATCACCTTC	360	
Qy	361	AAAAGTTTCAAAAGAACCTGAAGGATTTTCTGTGTTGAGATCCCGTTTGACTGCTGGAAG	420	
Db	361	GAAAGTTTCAAGAGAACCTGAAGGACTTCTGTGTTGATCCCTTTGACTGCTGGAG	420	
Qy	421	CCAGCCAGAGTAA	435	
Db	421	CCAGTCCAGGATGA	435	

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; Sequence 17, Application US/10410997
; Publication No. US20040126838A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF
; TITLE OF INVENTION: FSH
; FILE REFERENCE: 040853-01-5059
; CURRENT APPLICATION NUMBER: US/10/410,997
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-410-997-17

Query Match 76.1%; Score 331; DB 8; Length 435;
Best Local Similarity 85.1%; Pred. No. 7e-97;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy 1 ATGTGGCTGCAGAACTGCTTCTTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60
Db 1 ATGTGGCTGCAGAGCTGCTCTTGGGCACTGTGGGCTGCAGCATCTCTGCACCCGCC 60
Qy 61 CGCCAAACCCAGCCCTGCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db 61 CGCTCGCCAGCCCCAGCACGCGCCCTGGGAGCATGTGAATGCCATCAGAGGCCCGG 120
Qy 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 CGTCTCTGAACCTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180
Qy 181 TCTGAAACGTTTGACCGCGAGAGCTGACATGCTCGCTGCAGACTCGCCTGAAGCTGTACAA 240
Db 181 TCAGAAATGTTTGACTCCAGGAGCCGACCTGCCTACAGACCCGCTTGAGCTGTACAAG 240
Qy 241 CAGGCTTCGCGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGCTTCGCGGGGAGCCTCACCAAGCTCAAGGCCCTTGACCATGATGCCAGCCAC 300
Qy 301 TACAAGCAGACTGCCCCCACCCTCGAAACTTCTGTGCAACCCAGATGATCACCTTC 360
Db 301 TACAAGCAGACTGCCCCCACCCTCGAAACTTCTGTGCAACCCAGATGATCACCTTC 360
Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTGTTGAGATCCCGTTGACTGCTGGAG 420
Db 361 GAAAGTTTCAAAAGAACTGAAGACTTTCTGCTTGTATCCCTTTGACTGCTGGAG 420
Qy 421 CCAGCCCAAGATA 435

Db 421 CCAGTCAGAGTGA 435
RESULT 15
US-10-411-012-17
; Sequence 17, Application US/10411012
; Publication No. US20040132640A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryne
; TITLE OF INVENTION: GLYCOPEGLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5051
; CURRENT APPLICATION NUMBER: US/10/411,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-411-012-17

Query Match 76.1%; Score 331; DB 8; Length 435;
Best Local Similarity 85.1%; Pred. No. 7e-97;
Matches 370; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy 1 ATGTGGCTGCAGAACTGCTTCTTGGGCACTGTGGTTTACAGATGCCGCCACCCACC 60
Db 1 ATGTGGCTGCAGAGCTGCTCTTGGGCACTGTGGGCTGCAGCATCTCTGCACCCGCC 60
Qy 61 CGCCAAACCCAGCCCTGCTACTCGGCCCTGGCAGCATGTGGATGCCATCAAGAGGCCCTG 120
Db 61 CGCTCGCCAGCCCCAGCACGCGCCCTGGGAGCATGTGAATGCCATCAGAGGCCCGG 120
Qy 121 AGCCTTCTGAACAACAGTAGTGACACTGCTGTATCATGAATGAACAGTAGAAGTCGTC 180
Db 121 CGTCTCTGAACCTGAGTAGAGACACTGCTGTGAGATGAATGAACAGTAGAAGTCATC 180
Qy 181 TCTGAAACGTTTGACCGCGAGAGCTGACATGCTCGCTGCAGACTCGCCTGAAGCTGTACAA 240
Db 181 TCAGAAATGTTTGACTCCAGGAGCCGACCTGCCTACAGACCCGCTTGAGCTGTACAAG 240
Qy 241 CAGGCTTCGCGGGGAGCCTCATCAAGCTCGAAGGCCCTTGACCATGATGCCAGCCAC 300
Db 241 CAGGCTTCGCGGGGAGCCTCACCAAGCTCAAGGCCCTTGACCATGATGCCAGCCAC 300
Qy 301 TACAAGCAGACTGCCCCCACCCTCGAAACTTCTGTGCAACCCAGATGATCACCTTC 360
Db 301 TACAAGCAGACTGCCCCCACCCTCGAAACTTCTGTGCAACCCAGATGATCACCTTC 360
Qy 361 AAAAGTTTCAAAAAGAACTGAAGATTTCTGTGTTGAGATCCCGTTGACTGCTGGAG 420
Db 361 GAAAGTTTCAAAAGAACTGAAGACTTTCTGCTTGTATCCCTTTGACTGCTGGAG 420
Qy 421 CCAGCCCAAGATA 435

Db 361 GAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGTGCTTGTGTCATCCCTTTGACTGCTGGGAG 420
Qy 421 CCAGCCCAAGTAA 435
Db 421 CCAGTCCAGGAGTGA 435

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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:01:08 ; Search time 50 Seconds
(without alignments)
252.088 Million cell updates/sec

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Gap 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	587	77.3	144	1	US-08-436-890-11
4	587	77.3	144	1	US-08-451-213-11
5	586	77.2	144	1	US-08-284-393B-11
6	586	77.2	144	2	US-09-522-217-114
7	586	77.2	144	2	US-09-923-246-114
8	586	77.2	144	2	US-10-295-723-114
9	586	77.2	144	2	US-10-282-622-10
10	586	77.2	144	5	PTUS-08950-11
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12	586	77.2	334	2	US-09-555-165-11
13	584	76.9	144	2	US-08-759-628-6
14	578	76.2	143	2	US-09-617-594A-10
15	578	76.2	143	2	US-10-209-507-10
16	577	76.0	143	2	US-09-617-594A-8
17	577	76.0	143	2	US-10-209-507-8
18	576	75.9	144	1	US-08-259-696B-9
19	576	75.9	144	1	US-08-902-513-9
20	571	75.2	144	2	US-09-322-409-120
21	571	75.2	144	2	US-09-451-527-120
22	571	75.2	144	3	US-10-262-439-120
23	570.5	75.2	143	1	US-08-259-696B-10
24	570.5	75.2	143	1	US-08-902-513-10
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27	533	70.2	132	7	5229496-4	Patent No. 5229496
28	533	70.2	132	7	5391485-4	Patent No. 5391485
29	532	70.1	168	1	US-08-318-193-10	Sequence 10, Appl
30	532	70.1	782	1	US-09-146-283-4	Sequence 4, Appl
31	532	70.1	782	2	US-08-579-823A-4	Sequence 4, Appl
32	532	70.1	782	2	US-09-344-195-4	Sequence 4, Appl
33	531	70.0	127	7	5405952-2	Patent No. 5405952
34	531	70.0	131	7	5229496-2	Patent No. 5229496
35	531	70.0	301	2	US-08-469-318-142	Sequence 142, App
36	531	70.0	301	2	US-08-468-609A-142	Sequence 142, App
37	531	70.0	301	2	US-08-446-872A-142	Sequence 142, App
38	531	70.0	301	2	US-08-762-227A-142	Sequence 142, App
39	531	70.0	301	5	PCT-US95-01185-142	Sequence 142, App
40	527	69.4	127	1	US-08-318-193-2	Sequence 2, Appl
41	527	69.4	127	2	US-09-462-941-8	Sequence 8, Appl
42	527	69.4	127	7	5229496-15	Patent No. 5229496
43	527	69.4	128	2	US-08-469-318-160	Sequence 160, App
44	527	69.4	128	2	US-08-468-609A-160	Sequence 160, App
45	527	69.4	128	2	US-08-446-872A-160	Sequence 160, App

ALIGNMENTS

RESULT 1
US-09-589-460-9
; Sequence 9, Application US/09589460
; Patent No. 6645740
; GENERAL INFORMATION:
; APPLICANT: Bublrot, et al.
; TITLE OF INVENTION: Equine GM-CSF
; FILE REFERENCE: 454313-2334.1
; CURRENT APPLICATION NUMBER: US/09/589,460
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/138,843
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Equine sp.
US-09-589-460-9

Query Match	100.0%	Score 759	DB 2	Length 144
Best Local Similarity	100.0%	Pred. No. 1.7e-82		
Matches 144	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MWLQNLGTVVYVSMPTQPSVTRP	QHVDAIKALSLLNNSDSTAAMNETVEV	60
Db	1	MWLQNLGTVVYVSMPTQPSVTRP	QHVDAIKALSLLNNSDSTAAMNETVEV	60
Qy	61	SETFPAELTCLQTLKLYKQGLRSLIKLEGLPTMASHYKHCPTLETSCATQMITF	120	
Db	61	SETFPAELTCLQTLKLYKQGLRSLIKLEGLPTMASHYKHCPTLETSCATQMITF	120	
Qy	121	KSFKNLKDFLFEIPDCWKPAQK	144	
Db	121	KSFKNLKDFLFEIPDCWKPAQK	144	
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; Sequence 11, Application US/08133979A				
; Patent No. 5589582				
; GENERAL INFORMATION:				
; APPLICANT: Hawley, Robert J.				
; APPLICANT: Ponath, Paul D.				
; APPLICANT: Rosa, Margaret D.				
; APPLICANT: Monroy, Rodney L.				
; APPLICANT: Schacter, Bernice Z.				
; TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines Therei				
; NUMBER OF SEQUENCES: 24				

```
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
;; STREET: 6 Becker Farm Road
;; CITY: Roseland
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 07068
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch diskette
;; COMPUTER: IBM PC Compatible
;; OPERATING SYSTEM: MS-DOS 5.0
;; SOFTWARE: Word Perfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/133,979A
;; FILING DATE: October 8, 1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Herron, Charles J.
;; REGISTRATION NUMBER: 28,019
;; REFERENCE/DOCKET NUMBER: 61750-79
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 144 AMINO ACIDS
;; TYPE: AMINO ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: LINEAR
;; HYPOTHETICAL: YES
;; ANTI-SENSE: NO
;; US-08-133-979A-11

Query Match 77.3%; Score 587; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 5.7e-62;
Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 MWLQNLGLLVVYVSMPTPTQPSVTRPWQHVDAIKEALSLNNSSDTAAIMNETVVV 60
DB 1 MWLQNLGLLVVYVSMPTPTQPSVTRPWQHVDAIKEALSLNNSSDTAAIMNETVDV 60
QY 61 SETFDAELTCLQTRLKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120
DB 61 CEMFPDQPTCVQTRNLNLYKQGLRSLRLKSPLLAKHYEQHCPLTEETSCTQSTIF 120
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144
DB 121 KSFKDSLNLKFLFTIPFDCWGPVK 144

RESULT 3
US-08-436-890-11
; Sequence 11, Application US/08436890
; Patent No. 5858963
; GENERAL INFORMATION:
; APPLICANT: Hawley, Robert J.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Rosa, Margaret D.
; APPLICANT: Monroy, Rodney L.
; APPLICANT: Schacter, Bernice Z.
; TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines There
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.0
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;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436,890
;; FILING DATE: May 8, 1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Herron, Charles J.
;; REGISTRATION NUMBER: 28,019
;; REFERENCE/DOCKET NUMBER: 61750-139
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 201-994-1700
;; TELEFAX: 201-994-1744
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 144 AMINO ACIDS
;; TYPE: AMINO ACID
;; STRANDEDNESS: SINGLE
;; TOPOLOGY: LINEAR
;; HYPOTHETICAL: YES
;; ANTI-SENSE: NO
;; US-08-436-890-11

Query Match 77.3%; Score 587; DB 1; Length 144;
Best Local Similarity 76.4%; Pred. No. 5.7e-62;
Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 MWLQNLGLLVVYVSMPTPTQPSVTRPWQHVDAIKEALSLNNSSDTAAIMNETVVV 60
DB 1 MWLQNLGLLVVYVCSISAPTRPPSPVTRPWQHVDAIKEALSLNNSSDTAAVMNETVDV 60
QY 61 SETFDAELTCLQTRLKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120
DB 61 CEMFPDQPTCVQTRNLNLYKQGLRSLRLKSPLLAKHYEQHCPLTEETSCTQSTIF 120
QY 121 KSFKNLKDFLFEIPFDCWKPAQK 144
DB 121 KSFKDSLNLKFLFTIPFDCWGPVK 144

RESULT 4
US-08-451-213-11
; Sequence 11, Application US/08451213
; Patent No. 5863528
; GENERAL INFORMATION:
; APPLICANT: Hawley, Robert J.
; APPLICANT: Ponath, Paul D.
; APPLICANT: Rosa, Margaret D.
; APPLICANT: Monroy, Rodney L.
; APPLICANT: Schacter, Bernice Z.
; TITLE OF INVENTION: Enhancement of Xenograft Tolerance and Porcine Cytokines There
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/451,213
; FILING DATE: 26-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/133,979
; FILING DATE: October 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Herron, Charles J.
; REGISTRATION NUMBER: 28,019
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REFERENCE/DOCKET NUMBER: 61750-79
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
HYPOTHETICAL: YES
ANTI-SENSE: NO
US-08-451-213-11

Query Match
Best Local Similarity 77.3%; Score 587; DB 1; Length 144;
Matches 110; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 1 MWLQNLGLGTVVYSPAPTRQPSVTRPQWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQNLGLGTVVCSISAPTRPPSPVTRPQWQHVDAIKEALSLNNSSDTAAVMNETVDV 60

QY 61 SETPDABELTCLQTRKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120
DB 61 CEMFDPQPTCQTRNLKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120

QY 121 KSFKKNLKDFLFPIPCDWKPAQK 144
DB 121 KSFKDNLKFLFIPIPCDWGPVKK 144

RESULT 5
US-08-284-393B-11
Sequence 11, Application US/08284393B
Patent No. 569234
GENERAL INFORMATION:
APPLICANT: Zurawski, Sandra M.
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,393B
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 144 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-284-393B-11

Query Match
77.2%; Score 586; DB 1; Length 144;

Best Local Similarity 76.4%; Pred. No. 7.5e-62;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLGLGTVVYSPAPTRQPSVTRPQWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQNLGLGTVVCSISAPTRPPSPVTRPQWQHVDAIQEARRLLNLSRDTAAEMNETVEVI 60

QY 61 SETPDABELTCLQTRKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQPTCQTRLELYKQGLRSLIKLKGPLTMASHYKQHCPTLETSCATQIITF 120

QY 121 KSFKKNLKDFLFPIPCDWKPAQK 144
DB 121 ESFKNLKDFLFPIPCDWEPVQE 144

RESULT 6
US-09-522-217-114
Sequence 114, Application US/09522217
Patent No. 6307024
GENERAL INFORMATION:
APPLICANT: Presnell, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 114
LENGTH: 144
TYPE: PRT
ORGANISM: Homo sapiens
US-09-522-217-114

Query Match
77.2%; Score 586; DB 2; Length 144;
Best Local Similarity 76.4%; Pred. No. 7.5e-62;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLGLGTVVYSPAPTRQPSVTRPQWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQNLGLGTVVCSISAPTRPPSPVTRPQWQHVDAIQEARRLLNLSRDTAAEMNETVEVI 60

QY 61 SETPDABELTCLQTRKLYKQGLRSLIKLEGLPTMMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQPTCQTRLELYKQGLRSLIKLKGPLTMASHYKQHCPTLETSCATQIITF 120

QY 121 KSFKKNLKDFLFPIPCDWKPAQK 144
DB 121 ESFKNLKDFLFPIPCDWEPVQE 144

RESULT 7
US-09-923-246-114
Sequence 114, Application US/09923246
Patent No. 6605272
GENERAL INFORMATION:
APPLICANT: Presnell, Scott R.


```
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08950
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,393
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-08950-11

Query Match 77.2%; Score 586; DB 5; Length 144;
Best Local Similarity 76.4%; Pred. No. 7.5e-62;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLVVYVSMPTQPSVTRPQWQVDAIKELSLNNSSDTAAIMNETVEV 60
Db 1 MWLQNLGLLVVYVSMPTQPSVTRPQWQVDAIKELSLNNSSDTAAIMNETVEV 60
Qy 61 SETFDABELTCLQTRLELYKQGLRSLTKLKGPLTMMASHYKQHCPTLETSCATQITF 120
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMMASHYKQHCPTLETSCATQITF 120
Qy 121 KSFKNLKDFLFEPFDCWKPAQK 144
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 11
US-09-555-165-9
; Sequence 9, Application US/09555165
; Patent No. 686698
; GENERAL INFORMATION:
; APPLICANT: Kitamura, Toshio
; APPLICANT: Kojima, Tetsuo
; TITLE OF INVENTION: SIGNAL SEQUENCE TRAPPING METHOD
; FILE REFERENCE: 06501-061001
; CURRENT APPLICATION NUMBER: US/09/555,165
; CURRENT FILING DATE: 2000-05-28
; PRIOR APPLICATION NUMBER: JP 9/324912
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: PCT/JP98/05326
; PRIOR FILING DATE: 1998-11-26
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized human GM-CSF-human mpl
; OTHER INFORMATION: fusion protein sequence
US-09-555-165-11

Query Match 77.2%; Score 586; DB 2; Length 334;
Best Local Similarity 76.4%; Pred. No. 2.6e-61;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLVVYVSMPTQPSVTRPQWQVDAIKELSLNNSSDTAAIMNETVEV 60
Db 1 MWLQNLGLLVVYVSMPTQPSVTRPQWQVDAIKELSLNNSSDTAAIMNETVEV 60
Qy 61 SETFDABELTCLQTRLELYKQGLRSLTKLKGPLTMMASHYKQHCPTLETSCATQITF 120
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMMASHYKQHCPTLETSCATQITF 120
Qy 121 KSFKNLKDFLFEPFDCWKPAQK 144
Db 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 13
US-08-759-628-6
; Sequence 6, Application US/08759628
; Patent No. 6225446
; GENERAL INFORMATION:
; APPLICANT: Altmann, Scott W.
; APPLICANT: Rock, Fernando L.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMLIAN PROTEINS
```

```
;
;
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,628
; FILING DATE: 05-DEC-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/008,574
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0552Q
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 18..144
; OTHER INFORMATION: /note= "peptide of Figure 1"
US-08-759-628-6

Query Match 76.9%; Score 584; DB 2; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.3e-61;
Matches 110; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLVVYVSMPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
Db 1 MWLQNLGLLVVYVSMPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
Qy 61 SETFDAEELTCLQRLKLYKQGLRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDLQEPKLCIQRLKLYKQGLRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
Qy 121 KSFKNLKDFLFEIPFDCWKPAQ 144
Db 121 ESFKNLKDFLLVIFDCWEPQ 144

RESULT 14
US-09-617-594A-10
; Sequence 10, Application US/09617594A
; Patent No. 6541458
; GENERAL INFORMATION:
; APPLICANT: Audonnet, et al.
; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V
; FILE REFERENCE: 454313-3151.1
; CURRENT APPLICATION NUMBER: US/09/617,594A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/193,332
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: France 00 01761
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: France 99 09421
; PRIOR FILING DATE: 1999-07-16
```

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;
;
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Felis sp.
US-09-617-594A-10

Query Match 76.2%; Score 578; DB 2; Length 143;
Best Local Similarity 76.9%; Pred. No. 6.7e-61;
Matches 110; Conservative 9; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLVVYVSMPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
Db 1 MWLQNLGLLVVYVSMPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
Qy 61 SETFDAEELTCLQRLKLYKQGLRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDPEEPKLCIQRLKLYKQGLRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
Qy 121 KSFKNLKDFLFEIPFDCWKPAQ 143
Db 121 KNFKNLKDFLFNIPFDCWKPVK 143

RESULT 15
US-10-209-507-10
; Sequence 10, Application US/10209507
; Patent No. 6914134
; GENERAL INFORMATION:
; APPLICANT: Audonnet, et al.
; TITLE OF INVENTION: FELINE CALICIVIRUS GENES AND VACCINES IN PARTICULAR RECOMBINANT V
; FILE REFERENCE: 454313-3151.2
; CURRENT APPLICATION NUMBER: US/10/209,507
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 09/617,594
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/193,332
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: France 00 01761
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: France 99 09421
; PRIOR FILING DATE: 1999-07-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Felis sp.
US-10-209-507-10

Query Match 76.2%; Score 578; DB 2; Length 143;
Best Local Similarity 76.9%; Pred. No. 6.7e-61;
Matches 110; Conservative 9; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MWLQNLGLLVVYVSMPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
Db 1 MWLQNLGLLVVYVSMPTQPSVTRPQWHDVDAIKALSLNNSSDTAAIMNETVEV 60
Qy 61 SETFDAEELTCLQRLKLYKQGLRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
Db 61 SEMFDPEEPKLCIQRLKLYKQGLRSLIKLEGPLTMMASHYKQHCPTLETSCATQMITF 120
Qy 121 KSFKNLKDFLFEIPFDCWKPAQ 143
Db 121 KNFKNLKDFLFNIPFDCWKPVK 143

Search completed: May 25, 2006, 15:02:32
Job time : 51 secs
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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:12:58 ; Search time 177 Seconds
(without alignments)
376.853 Million cell updates/sec

Title: US-10-614-481-9
Perfect score: 759
Sequence: 1 MWLQNLGTVVYSGMPAPT.....XNLKDFLFEIPDCWKPAQK 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	759	100.0	144	5	US-10-614-481-9
2	586	77.2	144	3	US-09-923-246-114
3	586	77.2	144	4	US-10-295-723-114
4	586	77.2	144	4	US-10-282-623-110
5	586	77.2	144	4	US-10-131-985-15
6	586	77.2	144	4	US-10-116-275-217
7	586	77.2	144	4	US-10-456-780-10
8	586	77.2	144	4	US-10-411-037-18
9	586	77.2	144	4	US-10-609-346-20
10	586	77.2	144	4	US-10-411-026-18
11	586	77.2	144	4	US-10-447-315-19
12	586	77.2	144	4	US-10-410-962-18
13	586	77.2	144	4	US-10-411-049-18
14	586	77.2	144	4	US-10-659-684-114
15	586	77.2	144	4	US-10-410-930-18
16	586	77.2	144	4	US-10-410-997-18
17	586	77.2	144	4	US-10-411-012-18
18	586	77.2	144	4	US-10-287-994-18
19	586	77.2	144	4	US-10-659-295-27
20	586	77.2	144	4	US-10-410-913-18
21	586	77.2	144	4	US-10-666-122-3
22	586	77.2	144	4	US-10-666-122-5
23	586	77.2	144	5	US-10-688-845-83
24	586	77.2	144	5	US-10-787-442-114
25	586	77.2	144	5	US-10-901-417-15
26	586	77.2	144	5	US-10-410-980-18
27	586	77.2	144	5	US-10-951-239-8

28	586	77.2	144	5	US-10-410-897-18	Sequence 18, Appl
29	586	77.2	144	5	US-10-492-161-18	Sequence 18, Appl
30	586	77.2	144	5	US-10-880-101A-27	Sequence 27, Appl
31	586	77.2	144	5	US-10-775-204-447	Sequence 447, App
32	586	77.2	144	5	US-10-775-204-448	Sequence 448, App
33	586	77.2	144	5	US-10-775-204-540	Sequence 540, App
34	586	77.2	144	5	US-10-775-204-541	Sequence 541, App
35	586	77.2	144	6	US-11-174-398-10	Sequence 10, Appl
36	586	77.2	144	6	US-11-183-205-18	Sequence 18, Appl
37	586	77.2	610	3	US-09-783-708-1	Sequence 1, Appli
38	586	77.2	729	5	US-10-775-204-324	Sequence 324, App
39	584	76.9	144	4	US-10-081-963-20	Sequence 20, Appl
40	584	76.9	144	4	US-10-351-157-181	Sequence 181, App
41	584	76.9	144	4	US-10-352-554-166	Sequence 166, App
42	584	76.9	144	5	US-10-925-205-6	Sequence 6, Appli
43	584	76.9	144	5	US-10-937-658-3	Sequence 3, Appli
44	584	76.9	144	6	US-11-066-480-6	Sequence 6, Appli
45	584	76.9	144	6	US-11-201-384-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-614-481-9
; Sequence 9, Application US/10614481
; Publication No. US20050059121A1
; GENERAL INFORMATION:
; APPLICANT: Bublot, et al.
; TITLE OF INVENTION: Equine GM-CSF
; FILE REFERENCE: 454313-2334.1
; CURRENT APPLICATION NUMBER: US/10/614,481
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: US/09/589,460
; PRIOR FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/138,843
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 9
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Equine sp.
US-10-614-481-9

Query Match	100.0%;	Score 759;	DB 5;	Length 144;
Best Local Similarity	100.0%;	Pred. No. 3.1e-78;	Mismatches 0;	Indels 0; Gaps 0;
Matches 144;	Conservative			
Qy	1	MWLQNLGTVVYSGMPAPTROPSPVTRPQHVDAIKEALSLNNSSDTAAMNETVEVV	60	
Db	1	MWLQNLGTVVYSGMPAPTROPSPVTRPQHVDAIKEALSLNNSSDTAAMNETVEVV	60	
Qy	61	SETFDAELTCLQTRKLYKQGLRSLIKLEPLTNMASHYKQHCPTTLETSCATOMITF	120	
Db	61	SETFDAELTCLQTRKLYKQGLRSLIKLEPLTNMASHYKQHCPTTLETSCATOMITF	120	
Qy	121	KSFKNLKDFLFEIPDCWKPAQK	144	
Db	121	KSFKNLKDFLFEIPDCWKPAQK	144	

RESULT 2
US-09-923-246-114
; Sequence 114, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.

```

; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-114

Query Match 77.2%; Score 586; DB 3; Length 144;
Best Local Similarity 76.4%; Pred. NO. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0

Qy 1 MWLQNLILGTVVYMPAPTPQSPVTRPWOHDAKEALSLNNSDPTAAIMNTEVYV 60
Db 1 MWLQSLLLGTVVACISIPASPSPTQPEHVNIAIQEARLLNLSRDTAAENNEVVI 60
Qy 61 SETFDABELTCLQTRKLKYKQGLRGLSLKLEGPTMMASHYKQHCPTTLETSCATQMITF 120
Db 61 SEMFDLQETPCLQTRLELYKQGLRGLSLTKLGLPTMMASHYKQHCPTTETSCATQIITF 120

Qy 121 KSPKNNLKDPLFEIPFDCWKPAQK 144
Db 121 ESGFKNLKDPLFLVIPFDCWEPVQE 144

RESULT 3
US-10-295-723-114
; Sequence 114, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: No. US20030125524A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-723-114

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; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-15

Query Match      77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQSLLLGTVACISAPSPSPSTQWPHVNAIQEARRLLNLSRDTAAEMNETVEI 60

QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPETSCATQIITF 120

QY 121 KSFKKNLKDFLFEPFDCWKPAQK 144
DB 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 6
US-10-116-275-217
; Sequence 217, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116,275
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 217
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-275-217

Query Match      77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQSLLLGTVACISAPSPSPSTQWPHVNAIQEARRLLNLSRDTAAEMNETVEI 60

QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPETSCATQIITF 120

QY 121 KSFKKNLKDFLFEPFDCWKPAQK 144
DB 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 7
US-10-456-780-10
; Sequence 10, Application US/10456780
; Publication No. US20040009150A1
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; GENERAL INFORMATION:
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Hughes, Steven D.
; APPLICANT: Holly, Richard D.
; TITLE OF INVENTION: USE OF IL-21 IN CANCER AND
; FILE REFERENCE: 03-08
; CURRENT APPLICATION NUMBER: US/10/456,780
; CURRENT FILING DATE: 2003-06-06
; PRIOR FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-456-780-10

Query Match      77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVSMPTPTQPSVTRPQWQVDAIKEALSLNNSSDTAAIMNETVEV 60
DB 1 MWLQSLLLGTVACISAPSPSPSTQWPHVNAIQEARRLLNLSRDTAAEMNETVEI 60

QY 61 SETFDAELTCLQTRKLYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQMITF 120
DB 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTPETSCATQIITF 120

QY 121 KSFKKNLKDFLFEPFDCWKPAQK 144
DB 121 ESFKENLKDFLLVIPFDCWEPVQE 144

RESULT 8
US-10-411-037-18
; Sequence 18, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-411-037-18
Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYVSMPTQPSVTRPQWQHVDAIKEALSILNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYVSMPTQPSVTRPQWQHVDAIKEALSILNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQITTF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQITTF 120
QY 121 KSFKKNLKDFLFEIPFDCWKPAQK 144
DB 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 9
US-10-609-346-20
; Sequence 20, Application US/10609346
; Publication No. US20040063635A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Zailin
; APPLICANT: Fu, Yan
; TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLO
; FILE REFERENCE: ZYU-0603
; CURRENT APPLICATION NUMBER: US/10/609,346
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US 60/392,948
; PRIOR FILING DATE: 2002-07-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-609-346-20

Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYVSMPTQPSVTRPQWQHVDAIKEALSILNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYVSMPTQPSVTRPQWQHVDAIKEALSILNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQITTF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQITTF 120
QY 121 KSFKKNLKDFLFEIPFDCWKPAQK 144
DB 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 10
US-10-411-026-18
; Sequence 18, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
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US-10-411-026-18
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-18

Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYVSMPTQPSVTRPQWQHVDAIKEALSILNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYVSMPTQPSVTRPQWQHVDAIKEALSILNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQITTF 120
DB 61 SEMFDLQEPCTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQITTF 120
QY 121 KSFKKNLKDFLFEIPFDCWKPAQK 144
DB 121 ESFKNLKDFLLVIPFDCWEPVQE 144

RESULT 11
US-10-447-315-19
; Sequence 19, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heitsig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1676.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-19

Query Match
Best Local Similarity 77.2%; Score 586; DB 4; Length 144;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLILGTVVYVSMPTQPSVTRPQWQHVDAIKEALSILNNSSDTAAMNETVEV 60
DB 1 MWLQNLILGTVVYVSMPTQPSVTRPQWQHVDAIKEALSILNNSSDTAAMNETVEV 60
QY 61 SETFDAEELTCLQTRLELYKQGLRSLIKLEGPLTMASHYKQHCPTLETSCATQITTF 120
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Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTETSCATQIITF 120
QY 121 KSFKNLKDFLFEIPDCWKPAQ 144
:||||:||||:||||:||||:||||:
Db 121 ESFKNLKDFLVIFDCWEPVQE 144

RESULT 12
US-10-410-962-18
; Sequence 18, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-18

Query Match 77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLLLTGVVYSPAPPTROPSVTRPQWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MWLQSLLLLTGVVACISAPSPSTQPEWVHVAIQEARLLNLNLSRDTAAENNEIVEI 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 SETPDABELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTETSCATQIITF 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTETSCATQIITF 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 KSFKNLKDFLFEIPDCWKPAQ 144
:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 ESFKNLKDFLVIFDCWEPVQE 144
:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 13
US-10-411-049-18
; Sequence 18, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
```

```
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-049-18

Query Match 77.2%; Score 586; DB 4; Length 144;
Best Local Similarity 76.4%; Pred. No. 1.8e-58;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLLLTGVVYSPAPPTROPSVTRPQWQHVDAIKEALSLNNSSDTAAIMNETVEV 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MWLQSLLLLTGVVACISAPSPSTQPEWVHVAIQEARLLNLNLSRDTAAENNEIVEI 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 SETPDABELTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTETSCATQIITF 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 SEMFDLQPTCLQTRLELYKQGLRSLTKLKGPLTMASHYKQHCPTTETSCATQIITF 120
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 KSFKNLKDFLFEIPDCWKPAQ 144
:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 ESFKNLKDFLVIFDCWEPVQE 144
:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-10-659-684-114
; Sequence 114, Application US/10659684
; Publication No. US20040110932A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/659,684
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
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OM protein - protein search, using sw model

Run on: May 25, 2006, 15:13:17 ; Search time 14 Seconds
(without alignments)
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Title: US-10-614-481-9

Perfect score: 759

Sequence: 1 MWLQNLGLGTGVVYVSMPT.....KNLKDFLFEPDCKWPAQK 144

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 56051

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA_New.*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586	77.2	144	6	US-10-511-937-2460 Sequence 2460, Ap
2	586	77.2	144	7	US-11-183-218-18 Sequence 18, Appl
3	76	10.0	243	6	US-10-953-349-7275 Sequence 7275, Ap
4	76	10.0	285	6	US-10-953-349-7274 Sequence 7274, Ap
5	76	10.0	363	6	US-10-953-349-7273 Sequence 7273, Ap
6	71.5	9.4	293	6	US-10-953-349-20993 Sequence 20993, A
7	71.5	9.4	382	6	US-10-953-349-20992 Sequence 20992, A
8	70.5	9.3	734	7	US-11-293-697-3300 Sequence 3300, Ap
9	68.5	9.0	129	6	US-10-953-349-15150 Sequence 15150, A
10	68.5	9.0	364	6	US-10-953-349-18543 Sequence 18543, A
11	68.5	9.0	424	6	US-10-953-349-18542 Sequence 18542, A
12	68.5	9.0	438	6	US-10-953-349-18541 Sequence 18541, A
13	68.5	9.0	482	6	US-10-953-349-24953 Sequence 24953, A
14	67.5	8.9	442	6	US-10-953-349-13761 Sequence 13761, A
15	67.5	8.9	445	6	US-10-953-349-13760 Sequence 13760, A
16	67.5	8.9	447	6	US-10-953-349-13759 Sequence 13759, A
17	67	8.8	224	6	US-10-953-349-20916 Sequence 20916, A
18	67	8.8	265	6	US-10-953-349-20915 Sequence 20915, A
19	67	8.8	288	6	US-10-953-349-20914 Sequence 20914, A
20	66	8.7	1089	6	US-10-196-749-266 Sequence 266, App
21	65.5	8.6	202	6	US-10-953-349-27848 Sequence 27848, A
22	65	8.6	337	6	US-10-953-349-10265 Sequence 10265, A
23	64.5	8.5	113	6	US-10-953-349-15151 Sequence 15151, A
24	63.5	8.4	265	7	US-11-314-018-8 Sequence 8, Appl
25	63	8.3	206	6	US-10-196-749-394 Sequence 394, App

ALIGNMENTS

RESULT 1

US-10-511-937-2460
; Sequence 2460, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2460
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2460

Query Match 77.2%; Score 586; DB 6; Length 144;

Best Local Similarity 76.4%; Pred. No. 5.2e-53;
Matches 110; Conservative 15; Mismatches 19; Indels 0; Gaps 0;

QY 1 MWLQNLGLGTGVVYVSMPTQPSPVTRPQHVDAIKEALSLLNNSDPTAAIMNETVEV 60
Db 1 MWLQNLGLGTGVVYVSMPTQPSPVTRPQHVDAIKEALSLLNNSDPTAAIMNETVEV 60
QY 61 SETPDABELTCLQTRKLYKQGLRSLIKLEGPLTMMASHYKQHCPTTETSCATQMTIF 120
Db 61 SEMFDQBPCTCLQTRKLYKQGLRSLIKLEGPLTMMASHYKQHCPTTETSCATQMTIF 120
QY 121 KSFKNLKDFLFEPDCKWPAQK 144
Db 121 ESFKENLKDFLVLVPDCWEPVQE 144


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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18543
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18543

Query Match          9.0%; Score 68.5; DB 6; Length 364;
Best Local Similarity 22.4%; Pred. No. 8.6;
Matches 35; Conservative 18; Mismatches 40; Indels 63; Gaps 6;

QY 15 SMPAPTRQSPVTRPQWHD-----AIKEALSILN-----NSSDTAAIMNE 55
Db 138 SSPAPTKKPL-----WOHLSEBALLAKLDPSVAVSYRRALSSRNGLRNTLSRDVRSMSGSS 192
QY 56 TVEVVSSETDAEE-----LTCLOTFLKLYKQGLRSLIKLEGPLTMWASHYKQHCPTTL 109
Db 193 PLIFHSSSFSGKNSLCLSGTDRIVLYCTSLRG-----IRKTY 233
QY 110 ETSCATQMI-----TFKSPFKNLKDFL 131
Db 234 EDCSVRMILRGFMVAVDERDISMDSYRKELKDAL 269

RESULT 11
US-10-953-349-18542
; Sequence 18542, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18542
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18542

Query Match          9.0%; Score 68.5; DB 6; Length 424;
Best Local Similarity 22.4%; Pred. No. 10;
Matches 35; Conservative 18; Mismatches 40; Indels 63; Gaps 6;

QY 15 SMPAPTRQSPVTRPQWHD-----AIKEALSILN-----NSSDTAAIMNE 55
Db 198 SSPAPTKKPL-----WOHLSEBALLAKLDPSVAVSYRRALSSRNGLRNTLSRDVRSMSGSS 252
QY 56 TVEVVSSETDAEE-----LTCLOTFLKLYKQGLRSLIKLEGPLTMWASHYKQHCPTTL 109
Db 253 PLIFHSSSFSGKNSLCLSGTDRIVLYCTSLRG-----IRKTY 293
QY 110 ETSCATQMI-----TFKSPFKNLKDFL 131
Db 294 EDCSVRMILRGFMVAVDERDISMDSYRKELKDAL 329

RESULT 12
US-10-953-349-18541
; Sequence 18541, Application US/109533349
; Publication No. US20060107345A1
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; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18541
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-18541

Query Match          9.0%; Score 68.5; DB 6; Length 438;
Best Local Similarity 22.4%; Pred. No. 11;
Matches 35; Conservative 18; Mismatches 40; Indels 63; Gaps 6;

QY 15 SMPAPTRQSPVTRPQWHD-----AIKEALSILN-----NSSDTAAIMNE 55
Db 212 SSPAPTKKPL-----WOHLSEBALLAKLDPSVAVSYRRALSSRNGLRNTLSRDVRSMSGSS 266
QY 56 TVEVVSSETDAEE-----LTCLOTFLKLYKQGLRSLIKLEGPLTMWASHYKQHCPTTL 109
Db 267 PLIFHSSSFSGKNSLCLSGTDRIVLYCTSLRG-----IRKTY 307
QY 110 ETSCATQMI-----TFKSPFKNLKDFL 131
Db 308 EDCSVRMILRGFMVAVDERDISMDSYRKELKDAL 343

RESULT 13
US-10-953-349-24953
; Sequence 24953, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24953
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24953

Query Match          9.0%; Score 68.5; DB 6; Length 482;
Best Local Similarity 30.4%; Pred. No. 12;
Matches 21; Conservative 11; Mismatches 32; Indels 5; Gaps 2;

QY 44 NNSSDTAIMNETVEVVSSETDAEBELTCLOTFL--KLYKQGLRSLIKL--EGPLTWMA 98
Db 4 NNSNDAFMRNQNAAVQARTKAQNSVNLQLKIGCSHTGLTANLKLFEPPPLEYKP 63
QY 99 SHYKQHCPP 107
Db 64 PPEKEKCPP 72

RESULT 14
US-10-953-349-13761
; Sequence 13761, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
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; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13761
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13761

Query Match 8.9%; Score 67.5; DB 6; Length 442;
Best Local Similarity 29.7%; Pred. No. 14;
Matches 22; Conservative 14; Mismatches 27; Indels 11; Gaps 3;
Qy 46 SSDTAAINNETVEVVSETFDABELTCLO--TRLKLYKQGLRGLSLIKLEGPLTMMASHYK- 102
Db 183 SSVAASLVQDVTVTLATDPVPAYTFGCIQKATGSSLPQGLLG---LGRGPLSLLAQTQKL 239
Qy 103 -----QHCPTLET 111
Db 240 YQSTFSYCLPSFKT 253

RESULT 15
US-10-953-349-13760
; Sequence 13760, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13760
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-13760

Query Match 8.9%; Score 67.5; DB 6; Length 445;
Best Local Similarity 29.7%; Pred. No. 14;
Matches 22; Conservative 14; Mismatches 27; Indels 11; Gaps 3;
Qy 46 SSDTAAINNETVEVVSETFDABELTCLO--TRLKLYKQGLRGLSLIKLEGPLTMMASHYK- 102
Db 186 SSVAASLVQDVTVTLATDPVPAYTFGCIQKATGSSLPQGLLG---LGRGPLSLLAQTQKL 242
Qy 103 -----QHCPTLET 111
Db 243 YQSTFSYCLPSFKT 256

Search completed: May 25, 2006, 15:16:25
Job time : 14 secs

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